

REMARKS

Status of the Claims

Claims 11 and 13-22 are pending in the instant application. Claims 1-10, 12, and 23 have been canceled without prejudice or disclaimer of the subject matter claimed therein. Claims 19-22 have been withdrawn from examination as being drawn to a non-elected invention. Claims 11 and 13-18 are currently under examination.

Applicants thank the Examiner for re-grouping claims 17, 18, and 23 in Group I.

Should the Examiner find claim 17 allowable, we request the opportunity to amend claims 19-22 such that they would be dependent on claim 17 and consequently re-joined as well (see MPEP 821.04).

Amendments to the Claims

Claims 11, 16, and 17 have been amended.

Support for the amendment to claim 11 is found in canceled claim 12.

Support for the amendment to claim 16 is found in Example 1, wherein it shows that the nucleic acid encoding a protein of interest can be integrated into the gene encoding HtrA protease. Thus, the nucleic acid can be integrated, but it need not be integrated into the gene encoding the HtrA protease.

Support for the amendment to claim 17 is found in claim 11 and in claim 17, itself.

These amendments do not introduce prohibited new matter.

Rejection Under 35 U.S.C. § 112, Second Paragraph

Claims 11-18 and 23 have been rejected as being indefinite for failing to particularly point and distinctly claim the subject matter of the invention.

Claims 11, 16, and 23 have been rejected for reciting “HtrA protease” because it is not clear what is meant by the term. As shown on page 1, lines 30 and 31, HtrA protease is a housekeeping serine protease that degrades abnormally or incorrectly folded proteins exported by the bacteria. Pages 1-3 of the specification provide citations that refer to the protease, showing that the protease is well known by its name “HtrA protease.” Additionally, the specification, on page 8, lines 6-11, provides a definition for HtrA protease.

Claims 15 and 18 are rejected for reciting "PrtP protease." As shown on page 3, lines 34-39, and on page 4, lines 27-35, the term "PrtP protease" refers to a specific protease. Annex 2 and Buist *et al.* indicate that PrtP, a PIII type protease, is structurally and functionally distinct from HtrA protease. Moreover, Applicants have performed a search to show that PrtP and HtrA proteases are distinct proteins. Annex 1 provides the amino acid sequence of HtrA protease of *Lactococcus lactis*. Annex 2 provides the amino acid sequence of PrtP protease of *Lactococcus lactis*. Annex 3 provides a copy of a CDD search performed with the amino acid sequence of HtrA of *Lactococcus lactis* as the query sequence which confirm that PrtP and HtrA proteases are structurally distinct. Accordingly, the PrtP protease in claims 15 and 18 correctly refers to an additional protease.

Claim 13 is rejected for reciting various bacterial strains. Page 7, lines 8-12, and page 9, lines 18-22 provide a list of various Gram positive bacteria that produce the HtrA protease and can be used in the present invention. The preferred embodiment is a *Lactobacillus* strain. However, other Gram positive bacteria express the HtrA protease. The attached result of an internet search (Google) indicate that various bacteria express HtrA protease. Additionally, annexes 4-7, which contain the results of BLAST searches performed against available sequences of several Gram positive bacteria such as *Lactobacilli*, *Lactococci*, and *Streptococci*, confirm that various Gram positive bacteria express the HtrA protease. Thus, the bacterial strains encompassed by claim 13 could be used to practice the method of claim 11.

Accordingly, Applicants respectfully request withdrawal of this rejection.

Rejection Under 35 U.S.C. § 102(b)

A. Claims 23 and 11-15 are rejected under 35 U.S.C. § 102(b) as being anticipated by Bayles *et al.*

Claim 23 has been canceled and claims 11-15 have been amended to recite a step for recovering the protein and that the size of the genome of the bacterial strain is equal to or less than 3.2 Mb.

Bayles *et al.* disclose mutant *Listeria monocytogenes* comprising a *HtrA* gene. However, Bayles *et al.* do not disclose a method of using this mutant bacterium to produce an exported protein. Claims 11-15 are directed to a method of producing a desired protein comprising

culturing a Gram positive bacterial strain that expresses the protein and that has a genome of less than or equal to 3.2 Mb and recovering the protein exported from the bacterial strain.

Accordingly, Bayles *et al.* do not anticipate the claimed invention. Applicants respectfully request withdrawal of this rejection.

B. Claims 23 and 11-15 are rejected under 35 U.S.C. § 102(b) as being anticipated by Buist *et al.*

Claim 23 has been canceled and claims 11-15 have been amended to recite a step for recovering the protein and that the size of the genome of the bacterial strain is equal to or less than 3.2 Mb.

Buist *et al.* disclose a PrtP negative *Lactococcus lactis* strain. However, Buist *et al.* do not disclose a Gram positive bacterial strain that does not express a functional HtrA protease or the use of such a strain to produce a desired protein. As discussed above HtrA protease and PrtP protease are structurally and functionally distinct proteases. Accordingly, Buist *et al.* do not anticipate the claimed invention. Applicants respectfully request withdrawal of this rejection.

The Examiner notes that the prior art teaches multiple protease-deficient strains of *B. subtilis*. Applicants respectfully point out, unlike the bacterial strains used in the claimed invention, *B. subtilis* has a large genome of about 4.2 Mb that encodes several functional HtrA proteases such as YyxA, YkdA, and YvtB/Yirf and numerous other extracellular proteases.

C. Claims 23 and 11-15 are rejected under 35 U.S.C. § 102(b) as being anticipated by Smeds *et al.*

Claim 23 has been canceled and claims 11-15 have been amended to recite a step for recovering the protein and that the size of the genome of the bacterial strain is equal to or less than 3.2 Mb.

Smeds *et al.* disclose a strain of mutant *Lactobacillus helveticus* in which the *gusA* reporter gene was inserted downstream of the *htrA* promoter. The *gusA* reporter gene encodes β -glucuronidase. Although culturing the mutant *Lactobacillus helveticus* induces the *gusA* mRNA, culturing the mutant bacterial strain did not induce the expression of β -glucuronidase, the protein of interest (page 6152, col.1, second full paragraph). Thus, the cited reference does not and

could not teach recovering the protein of interest. Accordingly, Smeds *et al.* do not anticipate the claimed invention. Applicants respectfully request withdrawal of this rejection.

Rejection Under 35 U.S.C. § 103(a)

Claims 16, 17, and 18 are rejected under 35 U.S.C. § 103(a) as being unpatentable over Bayles *et al.* or Buist *et al.* as applied to claims 23 and 11-15 above, and further in view of any one of Dougan *et al.* or Georgiou *et al.*

Claim 16 is directed to a method of producing a protein of interest using Gram positive bacteria with a genome of less than or equal to 3.2 Mb and that does not express a functional HtrA protease. Claims 17 and 18 are directed to a Gram positive bacterial strain with a genome of less than or equal to 3.2 Mb and that does not express a functional HtrA protease. The small size of the genome leaves no room for the presence of other proteases of the HtrA family or for the presence of other proteases having a similar function. This ensures that no residual proteolytic activity remains after the single HtrA protease has been inactivated.

The deficiencies of Bayles *et al.* and Buist *et al.* are discussed above.

Dougan *et al.* teach Gram-negative bacteria having a mutation in the *degP* gene of the HtrA family for expressing a heterologous antigen. It seems that *degQ* and *degS* genes of the HtrA family are still intact and functional. Thus, the *htrA* protease gene of this bacteria is still functional with respect to the *degQ* and *degS* genes. Accordingly, Dougan *et al.* do not teach the use of Gram positive bacteria that have a genome of less than or equal to 3.2 Mb and that do not express a functional HtrA protease for producing a desired protein.

Similarly, Georgiou *et al.* disclose the use of mutant Gram negative bacteria that are multiply protease deficient for producing proteolytically sensitive polypeptides. Specifically, Georgiou *et al.* teach mutant Gram negative bacteria deficient in DegP, OmpT, and/or Protease III protease. It appears that since the *degQ* and *degS* genes of the HtrA are intact, the *htrA* gene must be functional. Accordingly, Georgiou *et al.* do not teach the use of Gram positive bacteria that have a genome of less than or equal to 3.2 Mb and that do not express a functional HtrA protease, which bacteria is used for producing a desired protein.

Applicants respectfully point out that Georgiou *et al.* stated that inactivation of a single protease is not sufficient to prevent the degradation of exported polypeptides (col. 2, lines 30-

40). Thus, Georgiou *et al.* teach inactivating multiple proteolytic enzymes. However, they point out that there is no assurance that disablement or deletion of any given protease or combination of proteases will result in a viable unchanged host cell or that such manipulation will avoid the precipitation of toxic events within the cell. Accordingly, although it is possible to create mutant organisms having deficiencies in more than three proteases because many Gram negative bacteria express at least seven or eight different proteases that degrade secreted polypeptides (col. 6, 1st paragraph), Georgiou *et al.* stated that deactivating a large number of proteolytic enzymes at some point will compromise the cell's viability (col. 6, 3rd paragraph).

Accordingly, there would not have been any reasonable expectation of success in obtaining the Gram positive bacteria of claims 17 and 18 or the method of using the Gram positive bacteria described in claim 16 by combining the cited references. Furthermore, there would not have been any motivation to combine the cited references since Bayles *et al.* and Buist *et al.* teach Gram positive bacteria while Dougan *et al.* and Georgiou *et al.* teach Gram negative bacteria. Gram positive bacteria are different from Gram negative bacteria in many aspects, including production of proteolytic enzymes. Applicants respectfully request withdrawal of the rejection.


Conclusion

The foregoing amendments and remarks are being made to place the application in condition for allowance. Applicants respectfully request entry of the amendments, reconsideration, and the timely allowance of the pending claims. A favorable action is awaited. Should the Examiner find that an interview would be helpful to further prosecution of this application, they are invited to telephone the undersigned at their convenience.

If there are any additional fees due in connection with the filing of this response, please charge the fees to our Deposit Account No. 50-0310. If a fee is required for an extension of time under 37 C.F.R. § 1.136 not accounted for above, such an extension is requested and the fee should also be charged to our Deposit Account.

Respectfully submitted,
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NiceProt View of Swiss-Prot: Q9LA06

Entry information

Entry name	HTRA_LACLA
Primary accession number	Q9LA06
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 40, October 2001
Sequence was last modified in	Release 40, October 2001
Annotations were last modified in	Release 41, February 2003

Name and origin of the protein

Protein name	Serine protease do-like htrA	
Synonyms	EC 3.4.21.- HtrAlI	
Gene name	HTRA or LL2136	
From	Lactococcus lactis (subsp. lactis) (Streptococcus lactis)	[TaxID: 1360]
Taxonomy	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.	

References

- [1] SEQUENCE FROM NUCLEIC ACID, AND CHARACTERIZATION.
STRAIN=IL1403;
MEDLINE=20177820; **PubMed=**10712686;
 Poquet I., Saint V., Seznec E., Simoes N., Bolotin A., Gruss A.;
 "HtrA is the unique surface housekeeping protease in Lactococcus lactis and is required
 for natural protein processing.";
 Mol. Microbiol. 35:1042-1051(2000).
- [2] SEQUENCE FROM NUCLEIC ACID.
STRAIN=IL1403;
MEDLINE=21235186; **PubMed=**11337471;
 Bolotin A., Wincker P., Mauger S., Jaillon O., Malarne K., Weissenbach J., Ehrlich S.D.,
 Sorokin A.;
 "The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis
 IL1403.";
 Genome Res. 11:731-753(2001).

Comments

- **FUNCTION:** DEGRADES ABNORMAL EXPORTED PROTEINS. NEEDED FOR THE PRO-PEPTIDE PROCESSING OF A NATURAL PRO-PROTEIN AND FOR MATURATION OF A NATIVE PROTEIN. RESPONSIBLE FOR THE HOUSEKEEPING OF EXPORTED PROTEINS.
- **SUBCELLULAR LOCATION:** Membrane-bound (*Probable*).
- **SIMILARITY:** Belongs to peptidase family S2C.

ANNEX 1

- **SIMILARITY:** Contains 1 PDZ/DHR domain.

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Cross-references

EMBL	AF155705; AAF61294.1; -. AE006442; AAK06234.1; -.
PIR	H86891; H86891.
MEROPS	S01.273; -.
InterPro	IPR009003; Cys_Ser_trypsin. IPR001478; PDZ. IPR001254; Peptidase_S1. IPR001940; Peptidase_S1C.
Pfam	PF00595; PDZ; 1. PF00089; trypsin; 1.
PRINTS	PR00834; PROTEASES2C.
SMART	SM00228; PDZ; 1.
PROSITE	PS50106; PDZ; 1.
Implicit links to	CMR; ProDom; HOBACGEN; BLOCKS; ProtoNet; ProtoMap; PRESAGE; DIP; ModBase; SWISS-2DPAGE.

Keywords

Hydrolase; Serine protease; Transmembrane; Complete proteome.

Features

Key	From	To	Length	Description
TRANSMEM	6	26	21	POTENTIAL.
DOMAIN	88	284	197	CATALYTIC.
DOMAIN	302	383	82	PDZ.
ACT_SITE	127	127		CHARGE RELAY SYSTEM (POTENTIAL).
ACT_SITE	157	157		CHARGE RELAY SYSTEM (POTENTIAL).
ACT_SITE	239	239		CHARGE RELAY SYSTEM (POTENTIAL).

Sequence information

Length: 408 AA

Molecular weight: 41648 Da

CRC64: 581B90B55A7DF851 [This is a checksum on the sequence]

ANNEX 1

10	20	30	40	50	60
MAKANIGKLL	LTGVVGAIA	LGGSATYQST	TNQSANNRS	NTTSTKVSNV	SVNVNTDVT
70	80	90	100	110	120
AIKKVNSNV	SVMNYQKDNS	QSSDFSSIFG	GNSGSSSSTD	GLQLSSEGS	VIYKKSGGDA
130	140	150	160	170	180
YVVTNYHVIA	GNSSLDVLLS	GGQVKASVV	GYDEYTDLAV	LKISSEHVKD	VATFADSSKL
190	200	210	220	230	240
TIGEPAAVG	SPLGSQFANT	ATEGILSATS	RQVTLTQENG	QTTNINAIQT	DAAINPGNSG
250	260	270	280	290	300
GALINIEGQV	IGITQSKITT	TEDGSTSVEG	LGFAIPSNDV	VNIINKLEAD	GKISRPAIGI
310	320	330	340	350	360
RMVDLSQLST	NDSSQLKLPS	SVTGGVVVYS	VQSGLPAAAS	GLKAGDVITK	VGDTAVTSST
370	380	390	400		
DLQSALYSHN	INDTVKVITY	RDGKSNTADV	KLSKSTSDLE	TSSPSSSN	

NiceProt View of Swiss-Prot: P15292

Entry information

Entry name	P3P_LACLC
Primary accession number	P15292
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 14, April 1990
Sequence was last modified in	Release 14, April 1990
Annotations were last modified in	Release 41, February 2003

Name and origin of the protein

Protein name	PIII-type proteinase [Precursor]	
Synonyms	EC 3.4.21.96 Lactocepin Cell wall-associated serine proteinase	
Gene name	PRTP	
From	Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris)	[TaxID: 1359]
Encoded on	Plasmid.	
Taxonomy	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.	

References

- [1] SEQUENCE FROM NUCLEIC ACID, AND SEQUENCE OF 188-197.
 STRAIN=SK11;
 MEDLINE=89340435; PubMed=2760036;
 Vos P., Simons G., Siezen R.J., de Vos W.M.;
 "Primary structure and organization of the gene for a procaryotic, cell envelope-located
 serine proteinase.";
 J. Biol. Chem. 264:13579-13585(1989).

Comments

- **FUNCTION:** PROTEASE WHICH BREAKS DOWN MILK PROTEINS DURING THE GROWTH OF THE BACTERIA ON MILK.
- **CATALYTIC ACTIVITY:** Endopeptidase activity with very broad specificity, although some subsite preference have been noted, e.g. large hydrophobic residues in the P1 and P4 positions, and Pro in the P2 position. Best known for its action on caseins, although it has been shown to hydrolyze hemoglobin and oxidized insulin B-chain.
- **SUBCELLULAR LOCATION:** Attached to the cell wall peptidoglycan by an amide bond (*Potential*).
- **SIMILARITY:** Belongs to peptidase family S8.

ANNEX 2

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Cross-references

EMBL	J04962; AAA03533.1; ALT_SEQ.
HSSP	P00782; 2SBT.
MEROPS	S08.019; -.
InterPro	IPR001899; Gram_pos_anchor. IPR003137; PA. IPR000209; Peptidase_S8.
Pfam	PF00746; Gram_pos_anchor; 1. PF02225; PA; 1. PF00082; Peptidase_S8; 1.
PRINTS	PR00723; SUBTILISIN.
TIGRFAMs	TIGR01167; LPXTG_anchor; 1.
PROSITE	PS50847; GRAM_POS_ANCHORING; 1. PS00136; SUBTILASE_ASP; 1. PS00137; SUBTILASE_HIS; 1. PS00138; SUBTILASE_SER; 1.
Implicit links to	ProDom; HOBACGEN; BLOCKS; ProtoNet; ProtoMap; PRESAGE; DIP; ModBase; SWISS-2DPAGE.

Keywords

Hydrolase; Serine protease; Cell wall; Peptidoglycan-anchor; Zymogen; Signal; Plasmid.

Features

Key	From	To	Length	Description
SIGNAL	1	33	33	
PROPEP	34	187	154	
CHAIN	188	1870	1683	PIII-TYPE PROTEINASE.
PROPEP	1871	1902	32	REMOVED BY SORTASE (<i>POTENTIAL</i>).
ACT_SITE	217	217		CHARGE RELAY SYSTEM (<i>BY SIMILARITY</i>).
ACT_SITE	281	281		CHARGE RELAY SYSTEM (<i>BY SIMILARITY</i>).
ACT_SITE	620	620		CHARGE RELAY SYSTEM (<i>BY SIMILARITY</i>).
SITE	1867	1871	5	LPXTG SORTING SIGNAL (<i>POTENTIAL</i>).
MOD_RES	1870	1870		AMIDE-LINKED TO CELL WALL (<i>POTENTIAL</i>).

ANNEX 2

Sequence information

Length: **1902 AA** [This is the length of the unprocessed precursor]

Molecular weight: **200550 Da** [This is the MW of the unprocessed precursor]

CRC64: **87CECBAA9345F9D3** [This is a checksum on the sequence]

10	20	30	40	50	60
MQRKKKGLSI	LLAGTVALGA	LAVLPVGEIQ	AKAAISQQTK	GSSLANTVTA	ATAKQAATDT
70	80	90	100	110	120
TAATTNQAI	A	TQLAAKGIDY	NKLNKVQQQD	IYVDVIVQMS	AAPASENGIL
130	140	150	160	170	180
QKETNKVIAA	QASVKA	AVEQ	VTQQTAGESY	GYVVNGFSTK	VRVVDIPK
190	200	210	220	230	240
AKVYYPTDAK	ANS	MANVQAV	WSNYKYKGE	G	TVVSVIDSGI
250	260	270	280	290	300
DVEKFTDTVK	HGRYFNSKVP	YGFNYADNND	TITDDKVDEQ	HGMHVAGIIG	ANGTGDDPAK
310	320	330	340	350	360
SVVGVAPEAQ	LLAMKVFSNS	D	TSAKTGSAT	VVSAIEDSAK	IGADV
370	380	390	400	410	420
DPELAAVQNA	NESGTA	AVIS	AGNSGTSGSA	TEGVNKDY	YG
430	440	450	460	470	480
SAENTDVITQ	AVTITDGTGL	QLGPETIQLS	SHDFTGSFDQ	KKFYIVKDAS	GNLSKGALAD
490	500	510	520	530	540
YTADAKGKIA	IVKRGEFSFD	DKQKYAQAAG	AAGLIIVNTD	GTATPMTSIA	LTTTFPTFGL
550	560	570	580	590	600
SSVTGQKLVD	WVTAHPDDSL	GVKITLAMLP	NQKYTEDKMS	DFTSYGPVSN	LSFKPDITAP
610	620	630	640	650	660
GGNIWSTQNN	NGYTNMSGTS	MASPF	FIAGSQ	ALLKQALNNK	NNPFYAYYKQ
670	680	690	700	710	720
KTVE	MNTAQ	P	INDINYN	NVI	VSPRRQ
730	740	750	760	770	780
FTSTD	KTFKL	TFTNRT	THEL	TYQMDS	NTDT
790	800	810	820	830	840
NAVY	TSATDP	NSGVLYDKKI	DGAAIKAGSN		

ANNEX 2

ITVPAGKTAQ	IEFTLSLPKS	FDQQQFVEGF	LNFKGSDGSR	LNLPYMGFFG	DWNDGKIVDS
850	860	870	880	890	900
LNGITYSPAG	GNFGTVPLLK	NKNTGTQYYG	GMVTDADGNK	TVDDQAIAFS	SDKNALYNDI
910	920	930	940	950	960
SMKYIYLLRNI	SNVQVDILDG	QGNKVTTLSS	STNRKKTYYN	AHSQQYIYYN	APAWDGTYYD
970	980	990	1000	1010	1020
QRDGNIKTAD	DGSYTYRISG	VPEGGDKRQV	FDVPFKLDSK	APTVRHVALS	AKTENGKTQY
1030	1040	1050	1060	1070	1080
YLTAEAKDDL	SGLDATKSVK	TEINEVTNLD	ATFTDAGTTA	DGYTKIETPL	SDEQAQALGN
1090	1100	1110	1120	1130	1140
GDNSAELYLT	DNASNATDQD	ASVQKPGSTS	FDLIVNGGGI	PDKISSTTTG	YEANTQGGGT
1150	1160	1170	1180	1190	1200
YTFSGTYPAA	VDGTYTDAQG	KKHDLNTTYD	AATNSFTASM	PVTNADYAAQ	VDLYADKAHT
1210	1220	1230	1240	1250	1260
QLLKHFDTKV	RLMAPTFTDL	KFNNGSDQTS	EATIKVTGTV	SADTKTVNVG	HTVAALDAQH
1270	1280	1290	1300	1310	1320
HFSVDVPVNY	GDNTIKVTAT	DKDGNTTTEQ	KTITSSYDPD	MLKKSVTFDQ	GVKFGTNKFN
1330	1340	1350	1360	1370	1380
ATSAKFYDPK	TGIATITGKV	KHPTTTLQVD	GKQIPIKDDL	TFSFTLDLGT	LGQKPFQVVV
1390	1400	1410	1420	1430	1440
GDTTQNKTQF	EALSFILDAV	APTLSDSST	DAPVYTNDPN	FQITGTATDN	AQYLSLSING
1450	1460	1470	1480	1490	1500
SSVASQYEDI	NINSGKPGHM	AIDQPVKLE	GKNVLTAVT	DSEDNTTKN	ITVYYEPKKT
1510	1520	1530	1540	1550	1560
LAAPTVPST	TEPAQTVTLT	ANAAATGETV	QYSADGGKTY	QDVPAAGVTI	TANGTFKFKS
1570	1580	1590	1600	1610	1620
TDLYGNESPA	VDYVVTNIKA	DDPAQLQAAK	QELTNLIASA	KTLSASGKYD	DATTTALAAA
1630	1640	1650	1660	1670	1680
TQKAQTALDQ	TNASVDSL TG	ANRDLQTAIN	QLAAKLPADK	KTSLLNQLQS	VKDALGTDLG
1690	1700	1710	1720	1730	1740

ANNEX 2

NQTDPSGTGKT FTAALDDLVA QAQAGTQTDD QLQATLAKIL DEVLAKLAEG IKAATPAEVG

1750	1760	1770	1780	1790	1800
NAKDAATGKT	WYADIADTLT	SGQASADASD	KLAHLQALQS	LKTKVAAAVE	AAKTVGKGDG

1810	1820	1830	1840	1850	1860
TTGTSDKGGG	QGTPAPAPGD	TGKDKGDEGS	QPSSGGNIPT	KPATTSTTTT	DDTTDRNGQL

1870	1880	1890	1900
TSGKGALPKT	GETTERPAFG	FLGVIVVSLM	GVLGLKRKQR EE

PubMed

Nucleotide

Protein

Structure

CDD

Taxonomy

Help?

CD: COG0265.1, DegQ, Query added

PSSM-Id: 10140

Source: Coq

Description: Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain [Posttranslational modification, protein turnover, chaperones]

Taxa: cellular organisms

Related: may span multiple domains

Status: Alignment from source

Created: 7-Oct-2002

Aligned: 135 rows

PSSM: 347 columns

Representative: Consensus

Proteins: [Click here for CDART summary of Proteins containing COG0265]

		10	20	30	40	50	60
consensus	1	LLVLAGLDLAVG-----	LLLIAAIAGG-----	-----	-----	-----	-----
query	1	-----	-----	-----	-----	-----	-----
gi 15616584	22	IGISAFIGAILGal-----	lvLFSVPALSGLgwlpyei--	dsgapteETGQLTEap	70		
gi 22001651	47	WFRPLLGIVIGSsla-----	lgiYTFTPLGNHdsqdtakq--	sssgqqtQSVTATSts	97		
gi 1731364	23	YFLSSLLGVIVGav-----	lmaFIMPYLSNEgldtg-----	aldgQ--QNNNgr	64		
gi 14194653	6	igkLLLTVGVGGAia-----	lgsSAIYQSTTNQs-----	-----	aNNRSNTts	44	
gi 15840667	141	AAAALGTPALAApaphgalagsgk	LGVRDVLFGKvsylalgilvalialvi	GGIGGVgr	200		
gi 15902042	14	LLVVIIVSFFSGal-----	gsFSITQLTQKs-----	-----	vNNSNNSti	50	
gi 15675945	10	sLSILLIGFLGgli-----	aiITFNNLYPHSp-----	-----	sKINSGKatt	46	
gi 16799397	122	YFLTALIGVIIggl-----	iIFFVAWDNGDnad-----	-----	ttS--NSNNkp	158	
		70	80	90	100	110	120
consensus	30	-----	GQR-----	LSFATAVEKVPAPVSIATGLTAKL-	-----	-----	-----
query	30	-----	-----	-----	-----	-----	-----
gi 15616584	71	ndietvnYAVn-----	SDVSQAVEKVDVAVV-GIVSMTNGs	-----	-----	-----	-----
gi 22001651	98	seskksSSSSafk-----	sedSKISDMVEDLSPAIV-GITNLQAQs	-----	-----	-----	-----
gi 1731364	65	esirtvnVSVn-----	NAVTKIVSNMSPAVV-GVVNIQKsd	-----	-----	-----	-----
gi 14194653	45	tkvsnvsVNVn-----	TDVTSIAKKVSNVSV-SVMNYQKNSqssd	-----	-----	-----	-----
gi 15840667	201	ktaevndAFTtskvtl1sttgna	QEPAGRFTKVAAAVADSVTIESV	-----	-----	-----	-----
gi 15902042	51	t---qtaYKNe-----	NSTTQAVNKVKDAVV-SVITYSANRqns	-----	-----	-----	-----
gi 15675945	47	s---nmvFNNT-----	TNTTKAVKAVQNAV-VSVINYQDNPsssl	snpytklfg	91		
gi 16799397	159	tkvekvsVNTt-----	SDVTKAVDKVKQDAVV-SVLNYQSSSsl	-----	-----	-----	-----
		130	140	150	160	170	180
consensus	59	SFF-PSDPP--LRSAEGLSGSFIIS--	SDG--	YIVTNNHVIAGAEITVTL-----	-----	-----	-----
query	90	-----	-----	-----	-----	-----	-----
gi 15616584	106	mFsSSEEE-----	EGTSGSVIYKkegDRA--	FIVTNEHVISGANQVev	-----	-----	-----
gi 22001651	142	slfGSSSSDssEDTESGSGSVIFKken	GKA--	YIVTNNHVIIEGASSLk	-----	-----	-----
gi 1731364	100	iWGESGE-----	AGSGSGVIYKndHSA--	YVVTNNHVIIEGASQIei	-----	-----	-----
gi 14194653	91	GNSGSSSSDtdgLQ-LSSEGS	SVIYKksgGDA--	YVVTNNHVIIEGASSLdv	-----	-----	-----
gi 15840667	247	-----	SDQE-----	GMQSGSVIVD--GRG--	YIVTNNHVIIEEAANN--	-----	-----
gi 15902042	89	Nd--DPTDTSqr--	ISSEGS	SVIYKndKEA--	YIVTNNHVIIEGASKVdi	-----	-----
gi 15675945	92	EGRsKENKDAeLS-IFSEGS	SVIYRkdGNSA--	YVVTNNHVIDGAKRIei	-----	-----	-----
gi 16799397	196	dgTtSSEKE-----	ASSGSGVIYKkanGKA--	YIVTNNHVIIEVADANKLev	-----	-----	-----
		190	200	210	220	230	240
consensus	103	-----	-----	-----	-----	-----	-----
query	140	-----	-----	-----	-----	-----	-----
gi 15616584	147	vLTGDSRLPAEVLGSDVFTDLAVLE	IDGSDVETVAEFGNSDLLSPGEPAIA	IGNPLGrf	206		
gi 22001651	140	slYDGETTAKVLGSDSLTDLAVL	QISDDHVTKVANFGSDSLRTGETVIA	IGDPLGkdL	249		
gi 1731364	140	sIKDGSRSVADLVGSDQLMDLAVL	RVKSKDIKAVADFGNSDKVKS	GEPVIAIGNPLGLEf	199		
gi 14194653	138	lLSGGQVKVASVVGyDEYTDLAVL	KISSEHVKDVA TFADSSKLTIGEP	PAIAVGSPLGsf	197		
gi 15840667	287	vFNDGKEVPANLVGRDPKTDLAVL	KVDNVLNLTVARLGDSKVRVGD	EVLA VGAP			
gi 15902042	133	rLSDGTVKVPGEIGVADTFSDIAV	VKISSEKVTVAEFGDSKLTVGETAIA	IGSPLGseY	192		
gi 15675945	139	lmaDGSVKGVEIGVADTYSLDIAV	VKISSDKIKTVAEFADSTKLVNGETAIA	IGSPLGteY	198		
gi 16799397	238	tftNGKKSEAKLLGTDEWDLAVLE	IDDKNVSTVATFGSDSLKLGEPAIA	IGSPLGteF	297		

ANNEX 3

		250	260	270	280	290	300			
	******			
consensus	159	GQTVTSGIVSALGR	---T-GVGSAGG	---YVNFIQTDAAINPGNSGGPLVNIDGEVV				208		
query	198	ANTATEGILSATS	RqvtlT-QENGQTT	---NINAIQTDAAINPGNSGGALINIEGQVI				251		
gi 15616584	207	SSSVTLGIISATER	---SiPIDLTGNgqidwQAEVLQTDAAINPGNSGGALVNIQGGQVI					262		
gi 22001651	250	SRTVTQGI	VS	GVDR---TvSMSTAGE---tSINVIQTDAAINPGNSGGPLLNTDGKIV				302		
gi 1731364	200	AGSVTQGVISGTER	---AiPVDSNGDgqpdwNAEVLQTDAAINPGNSGGALLNMDGKVI					255		
gi 14194653	198	ANTATEGILSATS	R---QvTLTQENGQt-tNINAIQTDAAINPGNSGGALINIEGQVI					251		
gi 15840667	345	RSTVTQGI	VSALHR---PvPLSGEGSdt-dtVIDAIQTDASINHGNSGGPLIDMDAQVI					399		
gi 15902042	193	ANTVTQGI	VSSSLNR---NvSLKSE	DGga--iSTKAIQTDTAINPGNSGGPLINIQQQVI				246		
gi 15675945	199	ANSVTQGI	VSSLSR---TvTLK	NEGet--vSTNAIQTDAAINPGNSGGPLINIEGQVI				252		
gi 16799397	298	SGSVTQGI	IISGLNR---AvPVD	TNGDgtedwEADVIQTDAAINPGNSGGALINIEGQVI				353		
		310	320	330	340	350	360			
	******			
consensus	209	GIN---	TAIIAPSGG	-----SSGIG	FAIPVNLVAPVLDELISKGVVRGYLGVIGE			256		
query	252	GITqski	TTTE	DGSTS-----VEGLG	FAIPSN	DVVNIINKLEADGKISR	PALGIRMV	303		
gi 15616584	263	GIN---	SMKIAQSt	-----VEGIG	FAIPSNLAI	PVIEDLEFYGDVQRPQM	GVAFR	309		
gi 22001651	303	GIN---	SMKISEDd	-----VEGIG	FAIPSN	DVKPIAEELLSKGQIERPYIGV	SML	349		
gi 1731364	256	GIN---	SMKIAESa	-----VEGIG	L	SI	PSKLVIPVIEDLERYGKVKRPF	LGIEMK	302	
gi 14194653	252	GIT---	QSKITTTedgs	---tsVEGLG	FAIPSN	DVVNIINKLEADGKISR	PALGIRMV	303		
gi 15840667	400	GIN---	TAGKSLsd	-----saSGLG	FAIPVNE	MKLVANSLIKDGKIVHPTLGISTR		447		
gi 15902042	247	GIT---	SSKIA	Tngg-----tsVEGLG	FAIP	PANDAINIIEQLEKNGKVTR	PALGIQMV	296		
gi 15675945	253	GIN---	SSKISSTPTg	snsgaVEGIG	FAIPSTDVIKIIKQLETNGE	VIRPALGISMV		308		
gi 16799397	354	GIN---	SMKISMEN	-----VEGIS	F	AIPSN	TVEPIIEQLET	KGEVERPSLGVSLR	400	
		370	380	390	400	410	420			
	******			
consensus	257	PLTADIA	-----LGLP	---VAAGAV	VLGLVPGS-----PAAKAGIKAGDIITAVNGK			300		
query	304	DLSQLST	-----NDSS	---QLKL	PSSVTGGVVYsvqsglPAASAGLKAGDVITKVGDT			354		
gi 15616584	310	SLSEIP	SfhweetLKLPe-dvKGG	VVITD	IVPMS-----PAETAGLRQYDVIVELNGE			361		
gi 22001651	350	DLEQVP	QnyqegtLGLFg	sqLNKGVYIRE	VASGS-----PAEKAGLKAEDIIIGLKGK			402		
gi 1731364	303	SLSDIA	Syhwde	tLKLpk-nVTNGAV	VMGVDAFS-----PAGKAGL	KELDVITEFDGY		354		
gi 14194653	304	DLSQLST	nds-sqLKL	Ps-sVTGG	VVVYVQSGSL-----PAASAGLKAGDVITKVGDT			354		
gi 15840667	448	--S--	VSn-----aIASGA	QVANVKAGS-----PAQKGGILENDVIVKVGNR				485		
gi 15902042	297	NLSNV	STsdi-rrLNIPs-nVTSG	IVIRS	VQSNM-----PAN-GHLEKYDVITKVDDK			346		
gi 15675945	309	NLNDL	STnal-sqINIPt-sVTGG	I	VVAE	VEKGM-----PAS-GKLAQYDVITEIDGK		358		
gi 16799397	401	DVD	TIPetqqkniLKLpd-sVDY	GAMVQ	VVSGS-----AADKAGLKQYDVIVELNGE			452		
		430	440	450	460					
	******			
consensus	301	PVASL	SDLVA	AVASNR--PGDE	VALKLLRGGKERELAVTLGDrSPLSAS			347		
query	355	AVTS	STDLQ	SALYSHN--INDT	VKVTTYR	DGKSNTADVklskstsdlet		401		
gi 15616584	362	DINDG	HEL	RKFLYTELn-IGDE	VEVTYYR	EGKKETTTTLT--VEQQSS		406		
gi 22001651	403	EIDT	GSEL	RNILYKDAK-IGDT	VEVKILRNGKEM	TKIKLDQ-KEEKTS		449		
gi 1731364	355	KVNDI	VDL	RKRLYQKK--VGDR	VKV	KFYRG	KEKSVDIKLSS-ADQLGS	400		
gi 14194653	355	AVTS	STDLQ	SALYSHN--INDT	VKVTTYR	DGKSNTADVklSK-STDLE		400		
gi 15840667	486	AVADS	DEFV	AVRQLA--IGQDA	PIEVVREGRH	VT	LT	VK	PDP-DST---	528
gi 15902042	347	EIAS	STDLQ	SALYNHS--IGDT	IKITYYRNGKEET	TSIKLNK-SSGDLE			392	
gi 15675945	359	TVNSI	SDLQ	SSLYGHD--INDT	IKVTFYRG	T	TKK	ADIKLTK-TTQDLT	404	
gi 16799397	453	KVTNS	MTLR	KILYGND	vkIGDKVKV	KYYRDGKEQSTDIKLEA-AKTTT			499	

ANNEX 4

BLASTP 2.2.6 [Apr-09-2003]

RID: 1067437801-292-1030821.BLASTQ3

Query= gi|15674118|ref|NP_268293.1| exported serine protease

[Lactococcus lactis subsp. lactis]

(408 letters)

Database: Unfinished Lactobacillus gasseri; Completed Lactobacillus plantarum WCFS1;

Completed Lactococcus lactis subsp. lactis;

Unfinished Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293;

Unfinished Oenococcus oeni MCW;

Completed Streptococcus agalactiae 2603V/R;

Completed Streptococcus agalactiae NEM316;

15,229 sequences; 4,501,851 total letters

Taxonomy reports

Sequences producing significant alignments:			Score (bits)	E Value
ref NP_268293.1	exported serine protease [Lactococcus lact...	576	e-165	
ref NP_689159.1	serine protease [Streptococcus agalactiae ...	303	5e-83	
ref NP_783901.1	serine protease HtrA [Lactobacillus planta...	283	5e-77	
ref ZP_00063134.1	COG0265: Trypsin-like serine proteases, ...	281	2e-76	
ref ZP_00069121.1	COG0265: Trypsin-like serine proteases, ...	272	7e-74	
ref ZP_00046803.1	COG0265: Trypsin-like serine proteases, ...	230	3e-61	
ref ZP_00070364.1	COG0265: Trypsin-like serine proteases, ...	181	2e-46	
ref ZP_00064063.1	COG0265: Trypsin-like serine proteases, ...	180	4e-46	
ref ZP_00070156.1	COG0750: Predicted membrane-associated Z...	45	2e-05	
ref NP_266705.1	UDP-N-acetylglucosamine 1-carboxyvinyltran...	35	0.034	
ref ZP_00046513.1	COG2996: Uncharacterized protein conserv...	33	0.097	
ref ZP_00063264.1	COG0750: Predicted membrane-associated Z...	33	0.13	
ref NP_785411.1	carboxy-terminal processing proteinase [La...	33	0.13	
ref NP_786668.1	extracellular protein [Lactobacillus plant...	32	0.28	
ref NP_268285.1	hypothetical protein [Lactococcus lactis s...	31	0.48	
ref NP_267651.1	sugar ABC transporter substrate binding pr...	30	1.1	
ref NP_687067.1	peptidase, M23/M37 family [Streptococcus a...	30	1.1	

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ref NP 784951.1	cell surface SD repeat protein precursor [...]	29	1.4
ref NP 786644.1	extracellular protein, gamma-D-glutamate-m...	29	1.4
ref NP 687090.1	alcohol dehydrogenase, propanol-preferring...	29	1.8
ref NP 267008.1	hypothetical protein [Lactococcus lactis s...	29	1.8
ref NP 734524.1	Unknown [Streptococcus agalactiae NEM316]	29	1.8
ref ZP 00064050.1	COG1364: N-acetylglutamate synthase (N-a...	28	2.4
ref ZP 00063238.1	COG1674: DNA segregation ATPase FtsK/Spo...	28	3.1
ref NP 735868.1	Unknown [Streptococcus agalactiae NEM316]	28	3.1
ref NP 784552.1	acetyltransferase (putative) [Lactobacillu...	28	3.1
ref ZP 00070200.1	COG1477: Membrane-associated lipoprotein...	28	3.1
ref ZP 00063415.1	COG1668: ABC-type Na+ efflux pump, perme...	28	4.1
ref NP 785643.1	endopeptidase La (putative) [Lactobacillus...	28	4.1
ref ZP 00069981.1	COG3051: Citrate lyase, alpha subunit [O...	28	4.1
ref ZP 00064376.1	COG1364: N-acetylglutamate synthase (N-a...	28	4.1
ref NP 688903.1	membrane-associated zinc metalloprotease, ...	28	4.1
ref NP 268318.1	hypothetical protein [Lactococcus lactis s...	27	5.3
ref ZP 00046283.1	COG0507: ATP-dependent exoDNase (exonucl...	27	5.3
ref ZP 00069420.1	COG3480: Predicted secreted protein cont...	27	5.3
ref ZP 00063200.1	COG0827: Adenine-specific DNA methylase ...	27	7.0
ref ZP 00062802.1	hypothetical protein [Leuconostoc mesent...	27	7.0
ref NP 687818.1	major facilitator family protein [Streptoc...	27	7.0
ref NP 688359.1	conserved hypothetical protein [Streptococ...	27	7.0
ref NP 688028.1	sensor histidine kinase, putative [Strepto...	27	7.0
ref NP 735272.1	Unknown [Streptococcus agalactiae NEM316]	27	7.0
ref NP 786635.1	extracellular protein [Lactobacillus plant...	27	7.0
ref ZP 00046678.1	COG4653: Predicted phage phi-C31 gp36 ma...	27	7.0
ref ZP 00046947.1	COG2931: RTX toxins and related Ca2+-bin...	27	7.0
ref ZP 00046780.1	COG3210: Large exoproteins involved in h...	27	7.0
ref ZP 00062638.1	COG4932: Predicted outer membrane protei...	27	9.1
ref NP 687888.1	exonuclease RexA [Streptococcus agalactiae...	27	9.1
ref NP 687383.1	3-oxoacyl-(acyl-carrier-protein) synthase ...	27	9.1

Alignments

>ref NP 268293.1 exported serine protease [Lactococcus lactis subsp. lactis]
Length = 408

Score = 576 bits (1484), Expect = e-165
Identities = 310/390 (79%), Positives = 310/390 (79%)

Query: 1 MAKANIGKLLLTGVVGAIALGGS AIYQXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 60
MAKANIGKLLLTGVVGAIALGGS AIYQ
Sbjct: 1 MAKANIGKLLLTGVVGAIALGGS AIYQSTTNQSANNRSNTTSTKVS NVSVNNTD VTS 60

Query: 61 AIKXXXXXXXXX MN YQKDNSQXXXXXXXXXXXXXXXXXXXXXXXXXXXXX EGSGVIYKKSGGDA 120
AIKK MN YQKDNSQ EGSGVIYKKSGGDA
Sbjct: 61 AIKKVSNSVSV MN YQKDNSQSSDFSSIFGGNSGSSSSTDGLQLSSEGS GVIYKKSGGDA 120

Query: 121 YVVTNYHVIAGNSSLDVLLSGGQVKVASVVG YDEYTDLAVLKISSEHV KDVATFADSSKL 180
YVVTNYHVIAGNSSLDVLLSGGQVKVASVVG YDEYTDLAVLKISSEHV KDVATFADSSKL
Sbjct: 121 YVVTNYHVIAGNSSLDVLLSGGQVKVASVVG YDEYTDLAVLKISSEHV KDVATFADSSKL 180

Query: 181 TIGEP AIVGSP LGSQFANTATEGILSATS RQVTLTQENGQTTNINAIQTDA AINP GNSG 240
TIGEP AIVGSP LGSQFANTATEGILSATS RQVTLTQENGQTTNINAIQTDA AINP GNSG
Sbjct: 181 TIGEP AIVGSP LGSQFANTATEGILSATS RQVTLTQENGQTTNINAIQTDA AINP GNSG 240

Query: 241 GALINIEGQVIGITQSKITTTEDGSTSVEGLGFAIP SN DVVNIINKLEADGKISR PALGI 300
GALINIEGQVIGITQSKITTTEDGSTSVEGLGFAIP SN DVVNIINKLEADGKISR PALGI
Sbjct: 241 GALINIEGQVIGITQSKITTTEDGSTSVEGLGFAIP SN DVVNIINKLEADGKISR PALGI 300

Query: 301 RMDLSQLSTNDSSQLKLPXXXXXXXXXXXXX LPAASAGLKAGDVITKVGDTAVTSST 360

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RMVDLSQLSTNDSSQLKLP LPAASAGLKAGDVITKVGDTAVTSST
 Sbjct: 301 RMVDLSQLSTNDSSQLKLPSSVTGGVVVYVQSGLPAASAGLKAGDVITKVGDTAVTSST 360
 Query: 361 DLQSALYSHNINDTVKVTYYRDGKSNTADV 390
 DLQSALYSHNINDTVKVTYYRDGKSNTADV
 Sbjct: 361 DLQSALYSHNINDTVKVTYYRDGKSNTADV 390

>ref|NP_689159.1| serine protease [Streptococcus agalactiae 2603V/R]
 ref|NP_736563.1| Unknown [Streptococcus agalactiae NEM316]
 Length = 409

Score = 303 bits (775), Expect = 5e-83
 Identities = 160/290 (55%), Positives = 201/290 (69%), Gaps = 7/290 (2%)

Query: 107 EGSQVYKSGGDAYVVTNYHVIAGNSSLDVLLSGGQKVKASVVGDEYTDLAVLKISSE 166
 EGSQVYK G +AYVVTN HVI G +++ L+ G K +VG D Y+DLAV+KI S+
 Sbjct: 105 EGSQVYKKGKGNAYVVTNNHVIDGAKQIEIQLADGSKAVGKLVGSDTYSDLAVVKIPSD 164
 Query: 167 HVKDVATFADSSKLTIGEPAlAVGSPGLGSQFANTATEGILSATS RQVTLTQENGQTTNIN 226
 V ++A FADSSKL IGE AIA+GSPGLG++AN+ T+GI+S+ R VT+T E GQT + N
 Sbjct: 165 KVSNIAEFADSSKLNIGETAIAIGSPGLGTEYANSVTQGIVSSLKRTVTMTNEEGQTVSTN 224
 Query: 227 AIQTDAAINPGNSGGALINIEGOVIGITQSKITTT-----EDGSTSVEGLGFAIPSN 280
 AIQTDAAINPGNSGGALINIEGOVIGI SKI++T + SVEG+GFAIPSN 280
 Sbjct: 225 AIQTDAAINPGNSGGALINIEGOVIGINSSKISSTSNQTSQSSGNSVEGMGFAIPSN 284
 Query: 281 VNIINKLEADGKISRPAIGRMVDLSQLSTNDSSQLKLPXXXXXXXXXXXXXXXXLPAASA 340
 V IIN+LE++G++ RPAIGI M LS L ++ S+LK+P +P A
 Sbjct: 285 VKIINQLESNGQVERPALGISMAGLSNLPSDVISKLKIPSNVTNGIVVASIQSGMP-AQG 343
 Query: 341 GLKAGDVITKVGDTAVTSSTDLQSALYSHNINDTVKVTYYRDGKSNTADV 390
 LK DVITKV D V S +DLQS LY H + D++ VT+YR T +
 Sbjct: 344 KLKKYDVITKVDDKEVVS PDLQSLLYGHQVGDSITVTFYRGENKQTVTI 393

>ref|NP_783901.1| serine protease HtrA [Lactobacillus plantarum WCFS1]
 Length = 420

Score = 283 bits (723), Expect = 5e-77
 Identities = 162/394 (41%), Positives = 214/394 (54%), Gaps = 14/394 (3%)

Query: 10 LLTGTVGGAIAGGSAIYQXXXXXXXXXXXXXXXXXXXXXXXXX---XXXXXXAIKKX 65
 L+ G++GG +A GG +Q +
 Sbjct: 14 LVAGLIGGGVAYGGIN YQNNNIATSSTSVPTGSNKSGSTSTTNVKNVSSQATKV FENN 73
 Query: 66 XXXXXXMNYQKDNSQXXX-----XXXXXXXXXXXXXXXXXXXXXXXXXEGSGVYKKS 118
 +N QK +S EGSQ+IYKKS
 Sbjct: 74 KAAVSVINLQKSSSSWSGILGGDDSSGSDSSSSSDSSSSKLEBYEGSGLIYKKS 133
 Query: 119 DAYVVTNYHVIAGNSSLDVLLSGGQKVKASVVGDEYTDLAVLKISSEHVKDVATFADSS 178
 AY+VTN HV++G+S++ V++S G K+ A +VG D TDLAVLKI+S V A+F +S
 Sbjct: 134 AAYIVTNNHVVSGSSAIRVIMSDGTLKSAKIVGTDVTDLAVLKINSKVTKTASFGNSD 193
 Query: 179 KLTIGEPAlAVGSPGLGSQFANTATEGILSATS RQVTLTQENGQTTN-INAIQTDAAINPG 237
 + +GE A+A+GSP+GS +A T T+GI+SA R V T +GQTT IQTD AIN G
 Sbjct: 194 NIKVGETALAI GSPMGSNYATTLTQGIISAKKRTVATTNTSGQTTGYATVIQDTAINSG 253
 Query: 238 NSGGALINIEGOVIGITQSKITTTEDGSTSVEGLGFAIPSNVNIINKLEADGKISRPA 297
 NSGG L NI GOVIGI K+ + G TSVEG+GFAIPSN+VV IIN+L G++ RPA
 Sbjct: 254 NSGGPLENIAGOVIGINSMKLASDNG-TSVEGMGFAIPSNVVKIINELVQKGEVVRPA 312

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Query: 298 LGIRMVDLSQLSTND-SSQLKLPXXXXXXXXXXXXXXXXXLPASAGLKAGDVITKVGDTAV 356
 LG+ DLS +S++D S LKLP PA +AGL DVIT++G V
 Sbjct: 313 LGVATYDLSNISSSDQKSVLKLPTSVTKGVVIMKTYSGSPAKAAGLTKYDVITELGGKKV 372

Query: 357 TSSTDLSALYSHNINDTVKVTYYRDGKSNTADV 390
 TS L+SALY+H++NDTV V YY +GK TA++
 Sbjct: 373 TSLATLRSALYAHSVNDTVTKYYHNGKLKTANM 406

>ref|ZP_00063134.1| COG0265: Trypsin-like serine proteases, typically periplasmic,
 contain C-terminal PDZ domain [Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293]
 Length = 379

Score = 281 bits (718), Expect = 2e-76
 Identities = 160/392 (40%), Positives = 214/392 (54%), Gaps = 23/392 (5%)

Query: 1 MAKANIGKLLLTGVVGGAIALGGSATYQXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 60
 M + + K LLTGV+ G + GG+ +Y
 Sbjct: 1 MVQPALTKLLTGVVGGAIALGGSATYQXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 59

Query: 61 AIKXXXXXXXXXMYQKDNSQXXXXXXXXXXXXXXXXXXXXXXXXXXXXXEGSGVIYKSGGDA 120
 A K +N+ K + EGSQVIYKK+ G A
 Sbjct: 60 AYNKVSDAVSVLNFTKSSQ-----GSYQESSEGSQVIYKKTGSA 100

Query: 121 VVVTNYHVIAGNSSLDVLLSGGQVKASVVGDEYTDLAVLKISSEHVKDVFADSSKL 180
 ++VTN/HVI G + + V+L G+KV A++VG D TDLAVLKI V A F DSSK+
 Sbjct: 101 FIVTNNHVIITGAQIQVMLHSGKKVTATLVGKDAMTDLAVLKIDGTDVTTTAQFGDSSKI 160

Query: 181 TIGEPAAVGSPLGSQFANTATEGILSATSQRQVTLTQENGQT-TNINAIQTDAAINPGNS 239
 T+GE +A+GSPLGS++A++ T+GI+SA R V T ENGQ IQTDAAINPGNS
 Sbjct: 161 TVGENVLAIGSPLGSEYASSVTQGIISAKKRLVEATSENGQNYGGSTVIQTDAAINPGNS 220

Query: 240 GGALINIEGQVIGITQSKITTTEDGSTSVEGLGFAIPSDVNIINKLEADGKISRPAIG 299
 GG-LIN GQVIGI K++T+ G TSVEG+GFAIPS+ VV+I+NKL DGK++RPA+G
 Sbjct: 221 GGFLINPAGQVIGINSMKLTSSSG-TSVEGMGFAIPSDQVVDIVNKLKVDGKVTTPAIG 279

Query: 300 IRMVDLSQLSTND-SSQLKLPXXXXXXXXXXXXXXXXXLPASAGLKAGDVITKVGDTAVTS 358
 I +++LS+++ ++ S LK+P PA AGLK DVI + V+S
 Sbjct: 280 ISLINLSEVTASEQKSTLKPDSVTGGVVMSLTNNGPADKAGLKKYDVIVGINGKKVSS 339

Query: 359 STDLSALYSHNINDTVKVTYYRDGKSNTADV 390
 DL+ LY H++ DT+ +TYY T V
 Sbjct: 340 QADLREELYKHSGLDITITLYYHQDTKQTVKV 371

>ref|ZP_00069121.1| COG0265: Trypsin-like serine proteases, typically periplasmic,
 contain C-terminal PDZ domain [Oenococcus oeni MCW]
 Length = 425

Score = 272 bits (696), Expect = 7e-74
 Identities = 160/390 (41%), Positives = 210/390 (53%), Gaps = 6/390 (1%)

Query: 6 IGKLLLTGVVGGAIALGGSATY-QXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAIKK 64
 I LL G++GG +A+G IY Q
 Sbjct: 29 IATALLAGLLGGVAVGAGYIYTQTTDFIGKSTGALS DGKTTIKAPTISGKSNATKVYNN 88

Query: 65 XXXXXXXXMYQKDNSQXXXXXXXXXXXXXXXXXXXXXXXXXXXXXEGSGVIYKSGGDAYVVT 124

ANNEX 4

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      +N Q +S                      EGSQVIYK + G AY+VT
Sbjct: 89 LKGAVSVINQATSSSSSTIYGDSSKSSSTSSSFSTLQTASEGSQVIYKDADGYAYIVT 148

Query: 125 NYHVIAGNSSLDVLLSGGQVKASVVGYDEYTDLAVLKISSEHVKDVFADSSSKLTIGE 184
      NYHVI+G + V+L GG KV A VG D TDLAVL+IS VK VA F +S+++ G+
Sbjct: 149 NYHVISGAKRIQVVLGGTKVVAKKVGSAMDLDLAVLRISGSDVKTVAQFGNSNQIKTGQ 208

Query: 185 PAIAVGSPGSGFANTATEGILSATSRSQVTLTQENGQTT--NINAIQTDAAINPGNSGGA 242
      +A+GSPLG+ +A++ TEGI+SA+ R V+ T E+G+T + AIQTDAAINPGNSGG
Sbjct: 209 TVLAIGSPGTDYASSVTEGIISASKRLVSNSTSESGKTYGDSIAIQTDAAINPGNSGGP 268

Query: 243 LNIIEGOVIGITQSKITTEDGSTSVGLGFAIPSNVNVNIINKLEADGKISRPAIGIRM 302
      L+N GOVIGI K+T T++G SVEG+GFAIPSN VV+IINKL GK+ RPAIG+ +
Sbjct: 269 LVNITSGOVIGINSQKLTTETDEGE-SVEGMGFAIPSNVTVSIINKLIYKGVVRPALGVEV 327

Query: 303 VDLSQLSTN-DSSQLKLPX-XXXXXXXXXXXXXXXXLPAASAGLKAGDVITKVGDTAVTSST 360
      VDLS++S++ LKLP PA AG+K DVI V V++
Sbjct: 328 VDLSEVSSDVVKTLKLPKVKGTGIVAGFSSDKSPAKKAGIKKYDVIVAVNGEKVSNLA 387

Query: 361 DLQSALYSHNINDTVKVTYYRDGKSNTADV 390
      D++ +Y + DTVK+TYYR T V
Sbjct: 388 DMRDIIYKLKVGDTVKITTYRASTEKTVMV 417

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>ref|ZP_00046803.1| COG0265: Trypsin-like serine proteases, typically periplasmic,
 contain C-terminal PDZ domain [Lactobacillus gasseri]
 Length = 666

Score = 230 bits (587), Expect = 3e-61
 Identities = 123/243 (50%), Positives = 162/243 (66%), Gaps = 2/243 (0%)

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Query: 107 EGSQVIYKSGGDAYVVTNYHVIAGNSSLDVLLSGGQVKASVVGYDEYTDLAVLKISSE 166
      EGSQVIY KS G Y+VTN HV++G+ + V+LS G+KV A VG D TDLAVL I +
Sbjct: 133 EGSQVIYKSNKGKGYVTNHYVSGSDEIQVILSNGKKVTAKKVGTDSETDLAVLTIDGK 192

Query: 167 HVKDVFADSSSKLTIGEPAIAVGSPGSGFANTATEGILSATSRSQVTLTQENGQTTN-I 225
      +V A F S L G+ IAVGSPGSG++A + T+GI+SA +R V +T GQ TN
Sbjct: 193 YVTQTAQGSSKNLEPGQVIAVGSPGSEYATSVTQGIISAKNRTVDVTNSAGQVTNQA 252

Query: 226 NAIQTDAAINPGNSGGALNIEGOVIGITQSKITTEDGSTSVGLGFAIPSNVNVNIIN 285
      IQTDAAINPGNSGG L+N GOVIGI K++++ DG T+VEG+GFAIPSN++VV+IIN
Sbjct: 253 TVIQTDAAINPGNSGGPLVNMGOVIGINSMLSSSSDG-TAVEGMGFAIPSNVTVSIIN 311

Query: 286 KLEADGKISRPAIGIRMVDLSQLSTNDSSQLKLPXXXXXXXXXXXXXXXXLPAASAGLKAG 345
      +L +GKI+RP LG+R+V + +L+ +L LP A AG+K+
Sbjct: 312 QLVKNGKITRPLKGVVSVDELTEYGRKKLGLPDSVKSGVYVASVTKNGSADKAGIKSH 371

Query: 346 DVI 348
      DVI
Sbjct: 372 DVI 374

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>ref|ZP_00070364.1| COG0265: Trypsin-like serine proteases, typically periplasmic,
 contain C-terminal PDZ domain [Oenococcus oeni MCW]
 Length = 301

Score = 181 bits (460), Expect = 2e-46
 Identities = 100/285 (35%), Positives = 148/285 (51%), Gaps = 12/285 (4%)

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Query: 10 LLTGVVGGAIALGGSALYQXXXXXXXXXXXXXXXXXXXX-XXXXXXXXXXAIKXXXX 67
 LL+ ++G + LG ++ A K
 Sbjct: 15 LLSAIIGATVVLGCFYLFYLAQAQNAKSSSIAAGMTKVVNLTGTSSSQATKAYNKVKN 74

Query: 68 XXXXXMNYQKDNSQXXXXX-----XXXXXXXXXXXXXXXXXXXXXEGSGVIYKKSGGDAYV 122
 NYQK +++ EG+G+IY+ G +Y+
 Sbjct: 75 AVVTVENYQKPSTEADYFFEWFGSQSGSSSSSSSTEDQLAAEGTGLIYETDGNYSYI 134

Query: 123 VTNHVIAGNSSLDVLLSGGQKVKASVVGDEYTDLAVLKISSEHVKDVFADSSKLT 182
 VTN HVI G + +++++ G KVKA ++G + D+AVL+ISS V TF +SSK+
 Sbjct: 135 VTNHVIKANEIEIIMANGTKVKAKLIGKNATKDIAVLRISASVTTTGTFTVNSSKVQA 194

Query: 183 GEPAIAGVSPGSGFANTATEGILSATSQVTLTQENGQTTNINAIQTDAAINPGNSGGA 242
 G+ +A+GSPLGS +A++ T GI+SAT+RQ+ + ++AIQTD A+NPGNSGG
 Sbjct: 195 GQQVLAIGSPGSDYASSLTSGIVSATNRQI-----DDSPIKLSAIQTDVALNPGNSGGP 249

Query: 243 LINIEGQVIGITQSKITTEDGSTSVEGLGFAIPSNDVNIINKL 287
 LIN+ G+VIGI KI++TEDGS VEG+ F+IPSN VV I +
 Sbjct: 250 LINMAGEVIGINSMKISSTEDGSEDVEGMSFSIPSNTVVATIKSI 294

>ref|ZP_00064063.1| COG0265: Trypsin-like serine proteases, typically periplasmic,
 contain C-terminal PDZ domain [Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293]
 Length = 253

Score = 180 bits (457), Expect = 4e-46
 Identities = 93/182 (51%), Positives = 129/182 (70%), Gaps = 3/182 (1%)

Query: 107 EGSQVIYKKSQGGDAYVVTNYHVIAGNSSLDVLLSGGQKVKASVVGDEYTDLAVLKISSE 166
 EGSQV+YK SGG AY++TN+HV+A + L ++ + G+K++A++VG D DLA+LK +
 Sbjct: 74 EGSQVYKISGGYAYIITNNHVVADSDQLITASGKKIQATIVGTDSSKDLALLKAKTT 133

Query: 167 HVKDVFADSSKLTIGEPALVSPGSGFANTATEGILSATSQVTLTQENGQTTNIN 226
 +K A+F ++ KL G+ +A+GSPLGS +A + T GI+SA R TL+ E ++
 Sbjct: 134 DIKTSASFNAKLLQSGQQVLAIGSPGSDYATSLTSGIVSAPRR--TLAEETGSSATT 191

Query: 227 AIQTDAAINPGNSGGALINIEGQVIGITQSKITTEDGSTSVEGLGFAIPSNDVNIINK 286
 AIQTDAAINPGNSGG LIN++GOV+GI SKI ++ DG TSVEG+GFAIP++ V I
 Sbjct: 192 AIQTDAAINPGNSGGPLENLKGOVVGINSKIASSTDG-TSVEGMGFAIPADIVQTFIKN 250

Query: 287 LE 288
 E
 Sbjct: 251 TE 252

>ref|ZP_00070156.1| COG0750: Predicted membrane-associated Zn-dependent proteases 1
 [Oenococcus oeni MCW]
 Length = 421

Score = 45.1 bits (105), Expect = 2e-05
 Identities = 26/56 (46%), Positives = 35/56 (62%), Gaps = 3/56 (5%)

Query: 336 PAASAGLKAGDVITKVGDTAVTSSTDLQSAALYSHNIND-TVKVITYYRDGKSNTADV 390
 PA GLK GDVITKV + +++ T L +A+ N+ D T+KV+Y R KS T V
 Sbjct: 218 PAMKQGLKKGDVITKVDSSKISNWTQLTTAI--ENVGDKTMKVSYYRGNKSRTVTV 271

>ref|NP_266705.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Lactococcus

ANNEX 4

lactis subsp. lactis]
Length = 427

Score = 34.7 bits (78), Expect = 0.034
Identities = 40/153 (26%), Positives = 71/153 (46%), Gaps = 14/153 (9%)

Query: 148 SVVGYDEYTDLAVLKISSEHVKDVATFADSSKLTIGEPAAVGSPLGSQF--ANTATEGI 205
+ + +D+ + K +SE +K A + SK+ +I V P+ ++ A + G
Sbjct: 65 TAISFDQEAQKIIAKSNSE-IKTTAPYEYVSKM---RASIVVMGPILARNGQARVSMPPG 120

Query: 206 LSATSRQVTLT---QENGQTTNINAIQTDAAINPGNSGGALINIEGQVIGITQSKI--T 259
S SR + L ++ G T NA +A + GA I ++ +G TQ+ I
Sbjct: 121 CSIGSRPIDLHLRGFEQMGATITQAGYIEAKAD--KLKGAHIYLDFPSVGATQNLILAA 178

Query: 260 TTEDGSTSVEGLGFAIPSNVDVNIINKLEADGK 292
T DG+T++E D+ N++NK+ A+ K
Sbjct: 179 TLADGTTTLENAAREPEIVDLANLLNKMGANVK 211

>ref|ZP_00046513.1| COG2996: Uncharacterized protein conserved in bacteria
[Lactobacillus gasseri]
Length = 297

Score = 33.1 bits (74), Expect = 0.097
Identities = 22/68 (32%), Positives = 37/68 (54%), Gaps = 4/68 (5%)

Query: 109 SGVIYKKSGGDAYVVTNYHVIA--GNSSLDVLLSGGQKVKASVVGYDEY--TDLAVLKIS 164
SG +Y+ ++V+T+ + +A S + L GQK+KA V+G +Y +L+VL
Sbjct: 157 SGTVYRNYEVGSFVITDQYYLAFVHKSEMFRLRLGQKIKARVIGVSQYGRNLNLSVLPRG 216

Query: 165 SEHVKDVA 172
E + D A
Sbjct: 217 FEEIDDDA 224

>ref|ZP_00063264.1| COG0750: Predicted membrane-associated Zn-dependent
proteases 1
[Leuconostoc mesenteroides subsp. mesenteroides ATCC
8293]
Length = 417

Score = 32.7 bits (73), Expect = 0.13
Identities = 18/56 (32%), Positives = 30/56 (53%), Gaps = 1/56 (1%)

Query: 335 LPAASAGLKAGDVITKVGDTAVTSSTDLSALYSHNINDTVKVTYYRDGKSNTADV 390
+PA AGLKAGD IT++ D T++ D + ++ + +T R+G +V
Sbjct: 212 MPADQAGLKAGDEITQI-DRVKTTTWDQVANAIGNSKESQLNITVLRNGHKKQVEV 266

>ref|NP_785411.1| carboxy-terminal processing proteinase [Lactobacillus
plantarum
WCFS1]
Length = 492

Score = 32.7 bits (73), Expect = 0.13
Identities = 20/56 (35%), Positives = 29/56 (51%), Gaps = 1/56 (1%)

Query: 336 PAASAGLKAGDVITKVGDTAVTSSTDLS-ALYSHNINDTVKVTYYRDGKSNTADV 390
PA AGLK D+I V +V T Q+ ++ I TVK+T R G++ T +
Sbjct: 147 PAKKAGLKPDKIIKAVNGKSVAGKTLTQAVSMMRGKIGTTVKLTIERSGQTFTVSL 202

ANNEX 4

>ref|NP_786668.1| extracellular protein [Lactobacillus plantarum WCFS1]
Length = 190

Score = 31.6 bits (70), Expect = 0.28
Identities = 32/141 (22%), Positives = 55/141 (39%), Gaps = 32/141 (22%)

Query: 187 IAVGSPLGSQFANTAT-----EGILSATS RQVLTQENGQTTNINAIQTDA----- 232
+ G PL Q A+T T E I T++ +TL Q G + I D+
Sbjct: 14 LMAGLPLVGQAADTETTTKAEVELIQDDTNKDITLDQAPGV SFGTEKITNDSKTYDAKNV 73

Query: 233 -----AINPGNSGGALINIEGQVI-----GITQSKITTTEDGSTSV-EGLGFA 274
NPGN+ G L+ ++G +T +++ T D + ++ + +
Sbjct: 74 TGD LKVTNPGNTDGWL VQVKGSKFMNADDTRELRGAALTFAQVNATADDANNISKAKAYK 133

Query: 275 IPSNDVVNIINKLEADGKISR 295
+ D II EA+ I +
Sbjct: 134 VDITDQNQIIMDAEANEIGIGK 154

>ref|NP_268285.1| hypothetical protein [Lactococcus lactis subsp. lactis]
Length = 428

Score = 30.8 bits (68), Expect = 0.48
Identities = 20/55 (36%), Positives = 28/55 (50%), Gaps = 1/55 (1%)

Query: 336 PAASAGLKAGDVITKVGDTAVTSSTDLQSALYSHNINDTVKVTYYRDGKSNTADV 390
PA +AGLKAGD I V T ++ + + S + +K+ R GKS T V
Sbjct: 225 PAYNAGLKAGDKIEAVNGTKTADWNNVVTEI-SGSKGKELKLEVSRSKGSETLSV 278

>ref|NP_267651.1| sugar ABC transporter substrate binding protein [Lactococcus lactis subsp. lactis]
Length = 483

Score = 29.6 bits (65), Expect = 1.1
Identities = 20/77 (25%), Positives = 35/77 (45%), Gaps = 1/77 (1%)

Query: 125 NYHVIAGNSSLDVLLSGGQKVKASVVG YDEYTDLAVLKISSEHV KDVATFADSSKLTIGE 184
NY + N++ + G K+ S +G+ +Y + +SS D+A FA +
Sbjct: 49 NYKELMANANKILEKKAGVKLDISYIGWGDY AQKMNIVVSSGEAYDIA-FAQDYATNAAK 107

Query: 185 PAIAVGSPLGSQFANTA 201
A A + L ++A TA
Sbjct: 108 GAFADLTDLAPKYAKTA 124

>ref|NP_687067.1| peptidase, M23/M37 family [Streptococcus agalactiae 2603V/R]
ref|NP_734500.1| Unknown [Streptococcus agalactiae NEM316]
Length = 299

Score = 29.6 bits (65), Expect = 1.1
Identities = 27/134 (20%), Positives = 50/134 (37%), Gaps = 7/134 (5%)

Query: 239 SGGALINIEGQVIGITQSKITTTEDGSTSVEGLGFAIPSNDVVNIINKLEADGKISRPAL 298
S G+ + + V I +ITT +G G+ +A+P+ ++ + ADG +
Sbjct: 20 SAGSRVLADTYVRPIDNGRIITGFGNGYPGHCGVDYAVPTGTIIRAV---ADGTVKFAGA 75

Query: 299 GIRMVDSLSQLSTNDSSQLKLPXXXXXXXLPAASAGLKAGDVITKVGDTAVTS 358
G ++ L+ N + + + +K GD+I VG T + +

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Sbjct: 76 GANFSWMTDLAGN---CVMIQHADGMHSGYAHMSRVVARTGEKVKQGDIIGYVGATGMAT 132
 Query: 359 STDLQSAALYSHNIN 372
 L N N
 Sbjct: 133 GPHLHFEFLPANPN 146

>ref|NP_784951.1| cell surface SD repeat protein precursor [Lactobacillus
 plantarum
 WCFS1]
 Length = 3360

Score = 29.3 bits (64), Expect = 1.4
 Identities = 42/145 (28%), Positives = 57/145 (39%), Gaps = 17/145 (11%)

Query: 164 SSEHVKDVFADSSSKLTIGEPAAVGSPLGS-----QFANTATEGILSATSRQVTLT 216
 S + V + SS LT+ A GS L AN T ++ +V +
 Sbjct: 1167 SYDAVDSAGLLSTSSSLTVTIKAGYTGSLLFQAVQGFSDLANWFTVYTFASNLAEVDVY 1226
 Query: 217 QENGQTTNINAIQTDAAINPGN-SGGALINIEGQVIGITQ-----SKIT-TTEDGS-TSV 268
 N TNI+ D INP N S G+ + Q T KIT TT D S ++
 Sbjct: 1227 SSNIPATNISIAGDDYVINPTNSSSGSNDKVTQSFTSTTNPENATGKITWTTSDSSIATI 1286
 Query: 269 EGLG-FAIPSNDVVNIINKL-EADG 291
 + G + SN V I + ADG
 Sbjct: 1287 DDSGLLTVVSNGTVTITATITNADG 1311

>ref|NP_786644.1| extracellular protein, gamma-D-glutamate-meso-diaminopimelate
 muropeptidase (putative) [Lactobacillus plantarum WCFS1]
 Length = 370

Score = 29.3 bits (64), Expect = 1.4
 Identities = 29/111 (26%), Positives = 42/111 (37%), Gaps = 3/111 (2%)

Query: 132 NSSLDVLLSGGQKVKASVVGYYDEYTDLAVLKISSEHVKDVFADSSSKLTIGEPAAVGS 191
 +SS+ S AS V T + SS V AT S+ + A +
 Sbjct: 144 SSSVAAQSSSTSTASASSVTSSASTSSVASQASSAVTSSATSQSSASQSSASQASQSST 203
 Query: 192 PLGSQFANTATEGILSATSRQVTLTQENGQTTNINAIQTDAAINPGNSGGA 242
 P+ S + TAT +ATS T+Q + +N + T A S A
 Sbjct: 204 PVASSTSTTATSTQSAATS---TSSQASSTASNTTSSSTTTATATAYSASA 251

>ref|NP_687090.1| alcohol dehydrogenase, propanol-preferring [Streptococcus
 agalactiae 2603V/R]
 Length = 338

Score = 28.9 bits (63), Expect = 1.8
 Identities = 19/69 (27%), Positives = 36/69 (52%), Gaps = 3/69 (4%)

Query: 112 IYKKS GG-DAYVVTNYHVIAGNSSLDVLLSGGQKVKASVVGYYDEYTDLAVLKISSEHVKD 170
 I +K+GG VVT +A N ++D + +GG V + EY +L+++K + ++
 Sbjct: 224 IQEKTGGCHGVVTVAVSKVAFNQAIDSVRAGGTVVAVGLP--SEYMELSIKTVLDGIRV 281
 Query: 171 VATFADSSK 179
 V + + K
 Sbjct: 282 VGSLVGTRK 290

>ref|NP_267008.1| hypothetical protein [Lactococcus lactis subsp. lactis]

ANNEX 4

Length = 1063

Score = 28.9 bits (63), Expect = 1.8
Identities = 53/272 (19%), Positives = 99/272 (36%), Gaps = 30/272 (11%)

Query: 120 AYVVTNYHVIAGNSSLDVLLSGGQKVKASVVGYDEYTDLAVLKISSEHVKDVFADSSK 179
A ++ + + N D + Q++ G E T + L S+ DVA A ++
Sbjct: 34 AIIIVSGTITDQNVKADTAIDSSQQIS----GITEVTSYSALASSTN--SDVA--ASQNQ 85

Query: 180 LTIGEPAIAGSPLGSQFANTATEGILSATSQRQVTLTQENGQTTNINAIQTDAAINPGNS 239
+ + + + + T TEGI S S E+ TT+ IQT P N+
Sbjct: 86 VAYEQASDQSSNKS LANTVETDTEGITSNVSDSSNSINESQNTTSTVVIQT-----PTNN 140

Query: 240 GGALINIEGQVIGITQSKITTTEDGSTSVEGLGFAIPSND-VVNIINKLEADGKISRPA 298
++ + S ++ ++GS S+ A S D V + + G +S +
Sbjct: 141 -----IVSLADSS-SSNDNGSNSILSSSNAADSVDSAVGSQSSTSSSGVLSESS- 188

Query: 299 GIRMVDLSQLSTNDSSQLKLPXXXXXXXXXXXXXXXXLPAASAGLKAGDVITKVGDTAVTS 358
+D S + SS++ L + ++T+ A +
Sbjct: 189 ---AIDSGIASVSQSSEMNLVGNSSASASSAAVASFTAILATNPSMVPMLTQALAAAPA 245

Query: 359 STDLSALYSHNINDTVKVTYYRDGKSNTADV 390
+T SA+ + + D V G S A++
Sbjct: 246 TTS-GSAILNTTLGDLVNQAISTVGISGLANI 276

>ref|NP_734524.1| Unknown [Streptococcus agalactiae NEM316]
Length = 338

Score = 28.9 bits (63), Expect = 1.8
Identities = 19/69 (27%), Positives = 36/69 (52%), Gaps = 3/69 (4%)

Query: 112 IYKKSGG-DAYVVTNYHVIAGNSSLDVLLSGGQKVKASVVGYDEYTDLAVLKISSEHVKD 170
I +K+GG VVT +A N ++D + +GG V + EY +L+++K + ++
Sbjct: 224 IQEKTGGCHGVVVTAVSKVAFNQAIDSVRAGGTVVAVGLP--SEYMELSIVKTVLDGIRV 281

Query: 171 VATFADSSK 179
V + + K
Sbjct: 282 VGSLVGTRK 290

>ref|ZP_00064050.1| COG1364: N-acetylglutamate synthase (N-acetylornithine
aminotransferase) [Leuconostoc mesenteroides subsp.
mesenteroides ATCC 8293]
Length = 344

Score = 28.5 bits (62), Expect = 2.4
Identities = 38/195 (19%), Positives = 77/195 (39%), Gaps = 22/195 (11%)

Query: 204 GILSATSQRQVTLTQENGQTTNINAIQTDAAINPGNSGGALINI-----EGQVIGITQSK 257
G+ + Q Q + +T +Q +N GN+ +I Q Q
Sbjct: 51 GVFTTNLVQAAPVQLDKKTIRNGQLQA-IIVNSGNANAVTGSIGVSHAESMQEFTAQQLN 109

Query: 258 ITTTEDGSTSVEGLGFAIPSNDVVNIINKLEADGKISRPA LGIRMVDLSQLSTNDSSQLK 317
I T+ G S +G +P + ++N I +L+ DG + A I D + S S ++
Sbjct: 110 IDTSLVGVASTGIIGKVLPIDKIINGIKQLKIDGDTNGFAHAIMTTDTKEKSITIQTSTIQ 169

Query: 318 LPXXXXXXXXXXXXXXXXLPAASAGLKAGDVITKVGDTAVTSSTDLSALYSHNINDTVKV 377
A +G+ ++ T +G +T+ ++ + L +++ V+
Sbjct: 170 GKIVTMSGV-----AKGSGMLHPNMATMLG--FITTDINIDAKLLQQALSEDVET 217

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Query: 378 TYR---DGKSENTAD 389
 ++ + DG ++T D
 Sbjct: 218 SFNQITIDGDTSTND 232

>ref|ZP 00063238.1| COG1674: DNA segregation ATPase FtsK/SpoIIIE and related proteins

[Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293]
 Length = 368

Score = 28.1 bits (61), Expect = 3.1
 Identities = 29/108 (26%), Positives = 42/108 (38%), Gaps = 7/108 (6%)

Query: 194 GSQFANTATEGILSATSRSQVTLTQENGQTTNINAIQTDAAINPGNSGGALINIEGQVIGI 253
 G+ +NT I+ Q + + T TD I NS A N + ++
 Sbjct: 253 GAFISNTDVTNIVEFVKSQQEVOYSDAMTV-----TDEEIAQDNSENADGNSDDELQFE 306

Query: 254 TQSKITTEDGSTSVEGLGFAIPSNVNIINKLEADGKISRPAIGIR 301
 + + STS+ F I N +I+ LEA G I PA G R
 Sbjct: 307 ALQFVIEQQASTSLQRRFRIGYNRAARLIDDLEAGGYIG-PADGSR 353

>ref|NP 735868.1| Unknown [Streptococcus agalactiae NEM316]
 Length = 414

Score = 28.1 bits (61), Expect = 3.1
 Identities = 35/165 (21%), Positives = 60/165 (36%), Gaps = 19/165 (11%)

Query: 137 VLLSGGQKVKAS--VVGYDEYTDLAVLKISSEHVKDVFADSSKLTIGEPPIAVGSPLG 194
 V + G K+ A +V YD T A ++ + VA ++ K T PA+ +
 Sbjct: 86 VTVKVGDKITAGQQLVQYDTTAAQAYDTANRQLNKVARQINNLTGSLPAMELSQSS 145

Query: 195 SQFANTATEGILSATSRSQVTLTQE-----NGQTTNINAIQTDAAINPGNSGGALINIEG 248
 S T+ AT+R Q N Q ++N DA + AL
 Sbjct: 146 SSSQGQGTQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKAL----- 200

Query: 249 QVIGITQSKITTEDGSTSVEGLGFAIPSNVNIINKLEADGKI 293
 + T++ T VE P++ ++ + +GK+
 Sbjct: 201 -----NDTVITSDVSGTVVEVNSDIDPASKTSQVLVHVATEGKL 239

>ref|NP 784552.1| acetyltransferase (putative) [Lactobacillus plantarum WCFS1]
 Length = 171

Score = 28.1 bits (61), Expect = 3.1
 Identities = 28/72 (38%), Positives = 40/72 (55%), Gaps = 13/72 (18%)

Query: 165 SEHVKD--ATFADSSKLTIGEPPIAVGSPLGSQFANTAT--EGI--LSATSRSQVTLTQE 218
 +E V DV A AD+++L +A+ + LG + +NT T EGI LS T Q + +
 Sbjct: 2 AEEVVDVRPAEVADAAQL-----LALLAQLGRE-SNTFTVDEGIEDLSETDEQAQIERI 54

Query: 219 NGQTTNINAIQT 230
 NG TTNI + T
 Sbjct: 55 NGTTNIIFVAT 66

>ref|ZP 00070200.1| COG1477: Membrane-associated lipoprotein involved in thiamine

biosynthesis [Oenococcus oeni MCW]
 Length = 358

ANNEX 4

Score = 28.1 bits (61), Expect = 3.1
Identities = 12/45 (26%), Positives = 24/45 (53%)

Query: 117 GGDAYVVTNYHVIAGNSSLDVLLSGGQKVKASVVGYDEYTDLAVL 161
GG+ YV+ H +G +V + + + S VGY +D+++
Sbjct: 210 GGNIIYVIGKSHPTSGTRDWNVGIQNPQNQSRGSSVGYVRESMSIV 254

>ref|ZP_00063415.1| COG1668: ABC-type Na⁺ efflux pump, permease component
[Leuconostoc
mesenteroides subsp. mesenteroides ATCC 8293]
Length = 438

Score = 27.7 bits (60), Expect = 4.1
Identities = 27/111 (24%), Positives = 47/111 (42%), Gaps = 8/111 (7%)

Query: 131 GNSSLDVLLSGGQKVKASVVGYDEYTDLAVLKISSEHVKDVATFAD--SSKLTIGE-PAI 187
GN++ ++ + G Q+V++ +V ++ D+ V I++E + A + LT+ + A
Sbjct: 80 GNTTPNIAVVGNGQEVRSILVQSEKELDIHVSNTITNEKKANTALQNEKLDGVLTVNKNEAT 139

Query: 188 AVGSPLGSQFANTATEGILSATSQRQVTLTQENGQTTNINAIQTDAAINPGN 238
P Q IL SR TQ + A QT + P N
Sbjct: 140 ITTQPKSEQIPKEKITAILGNLSRSQKATQ-----YGLTAEQTADLVQPYN 185

>ref|NP_785643.1| endopeptidase La (putative) [Lactobacillus plantarum WCFS1]
Length = 348

Score = 27.7 bits (60), Expect = 4.1
Identities = 14/42 (33%), Positives = 20/42 (47%)

Query: 342 LKAGDVITKVGDTAVTSSTDLSALYSHNINDTVKVITYYRDG 383
LK GD ITKV +++ Q + + V +TY R G
Sbjct: 149 LKVGDTITKVDGHHFNTASAYQHYIGKQGVGHRVTITYRRKG 190

>ref|ZP_00069981.1| COG3051: Citrate lyase, alpha subunit [Oenococcus oeni MCW]
Length = 449

Score = 27.7 bits (60), Expect = 4.1
Identities = 24/112 (21%), Positives = 45/112 (40%), Gaps = 4/112 (3%)

Query: 193 LGSQFANTATEGILSATSQRQVTLTQENGQTTNINAIQTDAAINPGNSGGALINIEGQVIG 252
LG + A + + + V ++G TNI + ++ S G L N V
Sbjct: 26 LGIKDLTLAPSSLTNVMNDMVVKAISKGTITNITSSGMRGSLGDAVSHGLLKN--PVVFR 83

Query: 253 ITQSKITTEDGSTSVEGLGFAIPSNVDVNIINKLEADGKISRPALGIRMVD 304
++ E+G ++ +P++D V N +E D +LG ++D
Sbjct: 84 SHGNRARAIEEGKIKIDVAFLGVPNSDEVGNANGMEGDAAFG--SLGYALMD 133

>ref|ZP_00064376.1| COG1364: N-acetylglutamate synthase (N-acetylornithine
aminotransferase) [Leuconostoc mesenteroides subsp.
mesenteroides ATCC 8293]
Length = 346

Score = 27.7 bits (60), Expect = 4.1
Identities = 28/138 (20%), Positives = 59/138 (42%), Gaps = 15/138 (10%)

Query: 255 QSKITTEDGSTSVEGLGFAIPSNVDVNIINKLEADGKISRPALGIRMVDLSQLSTNDSS 314

ANNEX 4

Q I T+ G S +G +P + ++N I +L+ DG + A I D + S S
 Sbjct: 49 QLNIDTSLVGVASTGIIGKVLPIIDKIINGIKQLKIDGDTNGFAHAIMTTDTKEKSITIQS 108
 Query: 315 QLKLPXXXXXXXXXXXXXXXXLPAASAGLKAGDVITKVGDTAVTSSTDLSALYSHNINDT 374
 ++ A +G+ ++ T +G +T+ ++ + L +++
 Sbjct: 109 TIQGIKIVTMSGV-----AKGSGMLHPNMTMLG--FITTDINIDAKLLQQALSED 156
 Query: 375 VKVTYYR---DGKSNTAD 389
 V+ ++ + DG ++T D
 Sbjct: 157 VETSFNQITIDGDTSTND 174

>ref|NP_688903.1| membrane-associated zinc metalloprotease, putative
 [Streptococcus
 agalactiae 2603V/R]
 ref|NP_736335.1| Unknown [Streptococcus agalactiae NEM316]
 Length = 419

Score = 27.7 bits (60), Expect = 4.1
 Identities = 14/31 (45%), Positives = 20/31 (64%)

Query: 336 PAASAGLKAGDVITKVGDTAVTSSTDLSAL 366
 PAASAGLK D I ++G V++ L +A+
 Sbjct: 212 PAASAGLKNDRILQIGSHKVSQVWQLTAAV 242

>ref|NP_268318.1| hypothetical protein [Lactococcus lactis subsp. lactis]
 Length = 342

Score = 27.3 bits (59), Expect = 5.3
 Identities = 13/40 (32%), Positives = 20/40 (50%)

Query: 342 LKAGDVITKVGDTAVTSSTDLSALYSHNINDTVKVTYYR 381
 L+ D IT V TSS D+ + + + D+V + Y R
 Sbjct: 151 LELADTITAVNGQQFTSSADMIAYVSKQKVGDSVTIEYTR 190

>ref|ZP_00046283.1| COG0507: ATP-dependent exoDNase (exonuclease V), alpha
 subunit -
 helicase superfamily I member [Lactobacillus gasserii]
 Length = 792

Score = 27.3 bits (59), Expect = 5.3
 Identities = 24/96 (25%), Positives = 43/96 (44%), Gaps = 11/96 (11%)

Query: 233 AINPGNSGGALIN----IEGQVIGITQSKITTT-----EDGSTSVEGLGFAIPSNDDV 281
 A N G + G +N + G ++ I QS ++T +D T L A +D+
 Sbjct: 201 ADNIGQALGIELNDPKRVRGAILSLQSALSTLGDTYVALDDLLTQAYDLVQASSYDDLA 260
 Query: 282 NIINKLEADGKISRPAIGIRMVDLSQLSTNDSSQLK 317
 N +N+L+ GK+ + + Q + S++LK
 Sbjct: 261 NSVNELQRQGVVSGDKAALQGIQTLEDISNELK 296

>ref|ZP_00069420.1| COG3480: Predicted secreted protein containing a PDZ domain
 [Oenococcus oeni MCW]
 Length = 364

Score = 27.3 bits (59), Expect = 5.3
 Identities = 14/44 (31%), Positives = 22/44 (50%)

ANNEX 4

Query: 342 LKAGDVITKVGDTAVTSSTDLSALYSHNINDTVKVTYYRDGKS 385
 +K GD ITKV +S Q L + + + V +T R+ K+
 Sbjct: 153 IKVGDTITKVDGKHFNNAGYQKYLAAMPVGEKVTLTVLRNNKT 196

>ref|ZP_00063200.1| COG0827: Adenine-specific DNA methylase [Leuconostoc
 mesenteroides
 subsp. mesenteroides ATCC 8293]
 Length = 329

Score = 26.9 bits (58), Expect = 7.0
 Identities = 20/66 (30%), Positives = 30/66 (45%), Gaps = 1/66 (1%)

Query: 251 IGITQSKITTTEGGSTSVGLGFAIPSNVDVNI-NKLEADGKISRPAIGRMVDLSQLS 309
 I + I ED ++ F PSNDVV II + ++ D + PA + + L+ L
 Sbjct: 26 ISYIDALIEILEDINSQTVHREFDKPSNDVVQIIQSTIDMDWSLLSPAERKALQLAVLK 85

Query: 310 TNDSSQ 315
 N Q
 Sbjct: 86 ANREDQ 91

>ref|ZP_00062802.1| hypothetical protein [Leuconostoc mesenteroides subsp.
 mesenteroides ATCC 8293]
 Length = 179

Score = 26.9 bits (58), Expect = 7.0
 Identities = 28/135 (20%), Positives = 52/135 (38%), Gaps = 5/135 (3%)

Query: 128 VIAGNSSLDVLLSGGQKVKASVVGDEYTDLAVLKISSEHVKDVAIFADSSKLITIGPAI 187
 + L L S GQ + A+ + + T + V ++ + K + + K G +
 Sbjct: 7 LFGSEKLSQLKSTGQ-INATRLARNNDTPVLVAPVTGDLQKITDSRDEPFKTKNGVMLV 65

Query: 188 AVGSPLGSQFANTATEGILSATSQVTLTQENGQTTNINAIQTDAAINPGNSGGALINIE 247
 L + + TE +T+ +TLT + QT + + T + G
 Sbjct: 66 PHSGNLMAPVSGIVTE----STNDYLTLTLDISEQTVTVTVVGTSNVVRLAQYGVGQQLHA 121

Query: 248 GQVIGITQSKITTTE 262
 G VIG T K+ + +
 Sbjct: 122 GDVIGTTNQKVLASD 136

>ref|NP_687818.1| major facilitator family protein [Streptococcus agalactiae
 2603V/R]
 Length = 383

Score = 26.9 bits (58), Expect = 7.0
 Identities = 13/26 (50%), Positives = 17/26 (65%)

Query: 2 AKANIGKLLLTGVVGGAIALGGSAY 27
 A NIGK L T +VG +A+G + IY
 Sbjct: 141 ASLNIGKALTTFIVGLVLAIGVNYIY 166

>ref|NP_688359.1| conserved hypothetical protein [Streptococcus agalactiae
 2603V/R]
 Length = 414

Score = 26.9 bits (58), Expect = 7.0
 Identities = 35/165 (21%), Positives = 59/165 (35%), Gaps = 19/165 (11%)

ANNEX 4

Query: 137 VLLSGGQKVKAS--VVGYDEYTDLAVLKISSEHVKDVFADSSKLTIGEPPIAVGSPGLG 194
 V + G K+ A +V YD T A ++ + VA ++ K T PA+
 Sbjct: 86 VTVKVGDKITAGQQLVQYDTTTAAQAYDTANRQLNKVARQINNLTGSLPAMESSDQSS 145

Query: 195 SQFANTATEGILSATSRSQVTLTQE-----NGQTTNINAIQTDAAINPGNSGGALINIEG 248
 S T+ AT+R Q N Q ++N DA + AL
 Sbjct: 146 SSSQGGGTQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVKNKAQKAL----- 200

Query: 249 QVIGITQSKITTTEDGSTSVEGLGFAIPSNDDVNNIINKLEADGKI 293
 + T++ T VE P++ ++ + +GK+
 Sbjct: 201 -----NDTVITSDVSGTVVEVNSDIDPASKTSQVLVHVHATEGKL 239

>ref|NP_688028.1| sensor histidine kinase, putative [Streptococcus agalactiae
 2603V/R]
 ref|NP_735501.1| Unknown [Streptococcus agalactiae NEM316]
 Length = 579

Score = 26.9 bits (58), Expect = 7.0
 Identities = 12/47 (25%), Positives = 28/47 (59%), Gaps = 1/47 (2%)

Query: 147 ASVVGYDEYTDLAVLKISSEHVKDVFADSSKLTIGEPPIAVGSPGL 193
 ++ G + +DL+++ + H+ D ++ A++ LTIG + +G P+
 Sbjct: 54 SNFTGVEIQSDLSIIPQTLNHIADQSSVANTRVLTIGVSGL-IGGPI 99

>ref|NP_735272.1| Unknown [Streptococcus agalactiae NEM316]
 Length = 383

Score = 26.9 bits (58), Expect = 7.0
 Identities = 13/26 (50%), Positives = 17/26 (65%)

Query: 2 AKANIGKLLLTGVVGGAIAGGSAIY 27
 A NIGK L T +VG +A+G + IY
 Sbjct: 141 ASLNIGKALTTFFIVGLVLAIGVNYIY 166

>ref|NP_786635.1| extracellular protein [Lactobacillus plantarum WCFS1]
 Length = 322

Score = 26.9 bits (58), Expect = 7.0
 Identities = 38/158 (24%), Positives = 65/158 (41%), Gaps = 14/158 (8%)

Query: 140 SGGQKVKASVVGYDEYTDLAVLKISSEHVKDVFADSSKLTIGEPPIAVGSPGLGSQ 196
 S G + ++ Y+ ++ I++ K+ A A D++ I L
 Sbjct: 104 SSGSGINVKILNYNGSNNITT--ITANQYKNAALTAGITDANIYVTSATPIDGSGALAGV 161

Query: 197 FANTATEGILSATSRSQVTLTQENGQT----TNINAIQ---TDAAINPGNSGGALINIEGQ 249
 +A A G S ++QVT Q+ T T N + TD+ +N +G A + +
 Sbjct: 162 YAAAYAKSGN-SLNTKQVTAAQDELSTLSGITQANKSKDGYTDSQLNNAVAG-AKKEMAQK 219

Query: 250 VIGITQSKITTTEDGSTSVEGLGFAIPSNDDVNNIINKL 287
 IT+++ITT + + L I +N IIN L
 Sbjct: 220 GSNITKNEITTIVNQITNNLTNVITNNQKTEIINLL 257

>ref|ZP_00046678.1| COG4653: Predicted phage phi-C31 gp36 major capsid-like
 protein
 [Lactobacillus gasserii]
 Length = 392

ANNEX 4

Score = 26.9 bits (58), Expect = 7.0
Identities = 16/64 (25%), Positives = 28/64 (43%), Gaps = 11/64 (17%)

Query: 140 SGGQKVKASVVGDEYTDL-----AVLKISSEHVKDVFADSSKLTIGEPAlA 188
+G KA + +D+ DL AV ++ + VK + D + I +P++
Sbjct: 248 AGSTAADALTFDDLIDLFYSLKAPYRQNAVFLMNDTIVKAIKMKDKNDQYIWQPSVQ 307

Query: 189 VGSP 192
VG P
Sbjct: 308 VGQP 311

>ref|ZP_00046947.1| COG2931: RTX toxins and related Ca2+-binding proteins
[Lactobacillus
gasseri]
Length = 1991

Score = 26.9 bits (58), Expect = 7.0
Identities = 30/113 (26%), Positives = 43/113 (38%), Gaps = 7/113 (6%)

Query: 114 KSGGDAYVVTNYHVIAGNSSLDVLLSGGQKVKASVVGDEYTDLAVLKISSEHVKDVFAT 173
K + G+ +T V AG L + S ++VKA YD + + V +AT
Sbjct: 1066 KDADGNYVAMTGNPVGNYAGTYLHLTKSAIEQVKADNSNYDFTSVNGEFTYITINAVNGIAT 1125

Query: 174 FADSSKLTIGEPAlA---VGSPLGSQFANTATEGILSATSQRQVTLTQENGQTT 223
+ SS T A+ V S G N G +S Q T + G T
Sbjct: 1126 LSGSSSKTYDGQAVTTAEVNSTNGDIIVNFTFPG---SSAQSTYVLQTGDYT 1174

>ref|ZP_00046780.1| COG3210: Large exoproteins involved in heme utilization or
adhesion
[Lactobacillus gasseri]
Length = 3692

Score = 26.9 bits (58), Expect = 7.0
Identities = 28/112 (25%), Positives = 45/112 (40%), Gaps = 7/112 (6%)

Query: 204 GILSATSQRQVTLTQENGQTTNINAIQTDAAINPGNSGGALINIEGQVIGITQSKITTED 263
G L +T +NG+ T + Q A+ + G I+ I QS T + D
Sbjct: 2225 GNLVTVDEDDGNITSQNGKITWNHESQFEAVPAIDHDGYIIS-----SINQSNSTASVD 2278

Query: 264 GSTSVEGLGFAIPSNDDVNIINKLEADGKISRPAIG-IRMVDLSQLSTNDSS 314
G T G P++ NI+ L + + A G I +D + T +S+
Sbjct: 2279 GQTGAVGTTETVTPNSQNGNIVITLTRNPDVPVAAQGSINYIDDTTGQTIESA 2330

>ref|ZP_00062638.1| COG4932: Predicted outer membrane protein [Leuconostoc
mesenteroides subsp. mesenteroides ATCC 8293]
Length = 508

Score = 26.6 bits (57), Expect = 9.1
Identities = 33/138 (23%), Positives = 50/138 (36%), Gaps = 29/138 (21%)

Query: 115 KSGGDAYVVTNYHVIAGNSSLD-----VLLSGGQKVKASVVGDEYTDLA 159
KSG D+ + ++ HV N D V L G KV + G L
Sbjct: 171 KSGSDSEINSDVHVYPKNEQTDAITKDLSDSKDLIVTLPDGSKVYNATYQKFGYQLQ 230

Query: 160 VLKISSEHVKDVFADSSKLTIGEPAlAV---GSPLGSQFANTATEGILSATSQRQVTLT 216
+ + KD D+ L I + A V G G+ + +AT+ T
Sbjct: 231 IAVPWNIADKDTFNVVDTPNLGIDDDATTVKVAGLTKGTDYTVSATDA-----T 279

ANNEX 4

Query: 217 QENGQTTNINAIQTDAAI 234
 +NG++ I T AA+
 Sbjct: 280 DKNGKSFKITFNPTAAAV 297

>ref|NP_687888.1| exonuclease RexA [Streptococcus agalactiae 2603V/R]
 Length = 1207

Score = 26.6 bits (57), Expect = 9.1
 Identities = 21/85 (24%), Positives = 33/85 (38%), Gaps = 8/85 (9%)

Query: 292 KISRPALGIRMVDLSQLSTNDSSQLKLPXXXXXXXXXXXXXXXXLPAASAGLKAGDVITKV 351
 KI P L I VD+ + T S KLP A+ G +++ ++
 Sbjct: 1010 KIYEPILDIEGVDMETITKTSVDFKLPDFSTSKKQ-----DPAALGSAVHELMQRI 1061

Query: 352 GDTAVTSSTDLSQALYSHNINDTVK 376
 ++ D+Q AL N +VK
 Sbjct: 1062 EMSSHVKMEDIQKALTEVNATSVK 1086

>ref|NP_687383.1| 3-oxoacyl-(acyl-carrier-protein) synthase II [Streptococcus
 agalactiae 2603V/R]
 ref|NP_734805.1| Unknown [Streptococcus agalactiae NEM316]
 Length = 410

Score = 26.6 bits (57), Expect = 9.1
 Identities = 30/148 (20%), Positives = 58/148 (39%), Gaps = 5/148 (3%)

Query: 117 GGDAYVVTNYHVIAGNSSLDVLLSGGQKVKASVVGDEYTDLAVLKISSEHVKDVATFAD 176
 GG +T+ IAG SL L + +AS+ + + S V + A+
 Sbjct: 189 GGAEAAITKF-AIAGFQSLTALSTTEDPSRASIPFDKDRNGFIMGEGSGMLVLESLEHAE 247

Query: 177 SSKLTIGEPAlAVGSPLGS-QFANTATEGILSATSQRQVTLTQENGQTTNINAIQTDAAIN 235
 TI + G+ + + EG+ + + Q+ L + N + +N +
 Sbjct: 248 KRGATILAEVVGYGNTCDAYHMTSPHPEGLGATKAIQLALVEANIKPEEVNIVNAHGTST 307

Query: 236 PGNSGG---ALINIEGQVIGITQSKITT 260
 P N G A++ G + ++ +K T
 Sbjct: 308 PANEGESQAIVAALGTDVPVSSTKSFT 335

Database: Unfinished Lactobacillus gasseri; Completed Lactobacillus
 plantarum WCFS1; Completed Lactococcus lactis subsp. lactis;
 Unfinished Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293;
 Unfinished Oenococcus oeni MCW; Completed Streptococcus agalactiae
 2603V/R; Completed Streptococcus agalactiae NEM316

Posted date: Oct 29, 2003 1:28 AM
 Number of letters in database: 4,501,851
 Number of sequences in database: 15,229

Lambda	K	H
0.308	0.128	0.338

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Hits to DB: 404,382
 Number of Sequences: 15229
 Number of extensions: 14371

ANNEX 4

Number of successful extensions: 43
Number of sequences better than 10.0: 10
Number of HSP's better than 10.0 without gapping: 4
Number of HSP's successfully gapped in prelim test: 6
Number of HSP's that attempted gapping in prelim test: 37
Number of HSP's gapped (non-prelim): 11
length of query: 408
length of database: 4,217,779
effective HSP length: 94
effective length of query: 314
effective length of database: 2,884,107
effective search space: 905609598
effective search space used: 905609598
T: 11
A: 40
X1: 16 (7.1 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 42 (21.7 bits)
S2: 57 (26.6 bits)

ANNEX 5

BLASTP 2.2.6 [Apr-09-2003]

RID: 1065207448-6660-583997.BLASTQ3

Query=

(408 letters)

Database: Completed Streptococcus mutans UA159;

1,531,058 sequences; 495,743,110 total letters

Taxonomy reports

		Score	E
Sequences producing significant alignments:		(bits)	Value
ref NP_722446.1	serine protease HtrA [Streptococcus mutans...	296	5e-82
ref NP_722143.1	putative transcriptional regulator [Strept...	28	0.36
ref NP_721869.1	putative UDP-N-acetylglucosamine 1-carboxy...	28	0.62
ref NP_721706.1	putative bacitracin synthetase [Streptococ...	27	0.81
ref NP_720929.1	putative polyribonucleotide nucleotidyltra...	27	1.1
ref NP_721524.1	putative ABC transporter, phosphate-bindin...	27	1.4
ref NP_722399.1	glucan-binding protein A, GbpA [Streptococ...	26	1.8
ref NP_721986.1	putative D-3-phosphoglycerate dehydrogenas...	26	2.4
ref NP_722066.1	putative 3-oxoacyl-(acyl-carrier-protein) ...	26	2.4
ref NP_722435.1	conserved hypothetical protein [Streptococ...	25	3.1
ref NP_721103.1	phosphoenolpyruvate:sugar phosphotransfera...	24	9.0
ref NP_720786.1	hypothetical protein [Streptococcus mutans...	24	9.0

Alignments

>ref|NP_722446.1| serine protease HtrA [Streptococcus mutans UA159]
Length = 402

Score = 296 bits (759), Expect = 5e-82
Identities = 153/286 (53%), Positives = 203/286 (70%), Gaps = 3/286 (1%)

Query: 107 EGSQVIYKKSGGDAIVVINYHVIAGNSSLDVLLSGGQKVKASVVGDEYTDLAIVLKISSE 166
EGSQVIYKK G AY+VTN+HV+ L+++++ G+KV +VG D Y+DLAV+KISS+

ANNEX 5

Sbjct: 107 EGSGLVIYKKGDSAYLVVNNHVVKDAEKLIMMANGKKVVGKLVGSDTYSDEAVIKISSK 166

Query: 167 HVKDVATFADSSKLTIGEPAlAVGSPLGSQFANTATEGILSATSrqVTLTQENGQTTNIN 226
+V VA FA+S K+ +GEPAIA+GSPLGS +AN+ TEGI+S+ SR VT ENG+T + N

Sbjct: 167 YVTTVAEFANSdKIKVGEPAIAIGSPLGSDYANSVTEGIVSSLSRTVTSQENGETISTN 226

Query: 227 AIQTDAAINPGNSGGALINIEGQVIGITQSKITTTEDGST--SVEGLGFAIPSNdVvNII 284
AIQTDAAINPGNSGGALINI+GOVIGI SKI ++ + ++ +VEG+GFAIPSNdVv+II

Sbjct: 227 AIQTDAAINPGNSGGALINIKGOVIGINSSKIASSNNSNSGVAVEGMGFAIPSNdVVSII 286

Query: 285 NKLEADGKISRPALGIRMVdLSQLSTNDSSQLKLPXXXXXXXXXXXXXXXXLPAASAGLKA 344
N+LE +G++ RPALGI M +LS+ ST+ LK+P +P A LK

Sbjct: 287 NQLEENGevVRPALGISMANLSEASTSGRDTLKIPSDVTSGIVVLSTQSGMP-ADGKLKK 345

Query: 345 GDVITKVGDTAVTSSTDLQsALYSHNINDTVKVTYRDGKSNTADV 390
DVIT++ V S +DLQS LY H D +K+T+YR+ T ++

Sbjct: 346 YDVITEIDGKKVASISDLQsILYKHKKGDKIKLTFYREKDKQTVEI 391

>ref|NP_722143.1| putative transcriptional regulator [Streptococcus mutans UA159]

Length = 261

Score = 28.5 bits (62), Expect = 0.36

Identities = 34/128 (26%), Positives = 51/128 (39%), Gaps = 26/128 (20%)

Query: 193 LGSQFANTATEGILSATSrqVTLTQENGQTTNINAIQTDAAIN---PGNSGGALINIEGQ 249
+G Q N TE L T R+ T T + + + + AAI GN G ++

Sbjct: 154 VGIQLLNlQTen-LEETIRKQTAINMAINTLSYSEMKAvaAILNELDGNegRLTASVIAD 212

Query: 250 VIGITQSKITTTEDGSTSVEGLGFAIPSNdVvNIINKLEADGKISRPALGIRMVdLSQLS 309
IGIT+S I VN + KLE+ G I +LG++ L ++

Sbjct: 213 RIGITRSVI-----VNALRKLESAGIIESRSLSGMKGTYLKVIN 250

Query: 310 TNDSSQLK 317
+LK

Sbjct: 251 EGIFDKLK 258

>ref|NP_721869.1| putative UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Streptococcus mutans UA159]

Length = 423

Score = 27.7 bits (60), Expect = 0.62

Identities = 34/146 (23%), Positives = 64/146 (43%), Gaps = 10/146 (6%)

Query: 150 VGYDEYTDLAVLKISSEHVKDVATFADSSKLTIGEPAlAVGSPLGSQ--FANTATEGILS 207
V +DE + ++ + + + DVA + S++ +I V P+ ++ A + G +

Sbjct: 66 VDFDEERNQILVdATGD-ILDVAPYeyVSQM---RASIVVLGPILARNGHAKVSMPPGGCT 121

Query: 208 ATSRQVTLTQENGQTTNINAIQT--DAAINPGNSGGALINIEGQVIGITQSKI--TTTED 263
SR + L + + QT D GA I ++ +G TQ+ + T D

Sbjct: 122 IGSRPIDLHLKGLEAMGAKIQQTGGDITATADRLKGANIYMDFPsVGATQNLmMAATLAD 181

Query: 264 GSTSVEGLGFAIPSNdVvNIINKLEA 289
G+T +E D+ N++NK+ A

Sbjct: 182 GTTIIENAAREPEIVDLANLLNKMGa 207

ANNEX 5

>ref|NP_721706.1| putative bacitracin synthetase [Streptococcus mutans UA159]
Length = 1455

Score = 27.3 bits (59), Expect = 0.81
Identities = 20/63 (31%), Positives = 29/63 (46%), Gaps = 3/63 (4%)

Query: 119 DAYVVTNYHVIAGNSSLDVLLSGGQKVKASVVGYYDEYT-DLAVLKISSEHVKDVATFADS 177
D V Y V G +D ++S K+K + Y E T +L S E H D+ T +
Sbjct: 887 DQVKVNGYRVELGE--IDSIIKMSKIKRAKTIYQEETGNLIAFCESKEHCSDIETRKEL 944

Query: 178 SKL 180
SK+
Sbjct: 945 SKI 947

>ref|NP_720929.1| putative polyribonucleotide nucleotidyltransferase (general stress

protein 13) [Streptococcus mutans UA159]
Length = 130

Score = 26.9 bits (58), Expect = 1.1
Identities = 13/25 (52%), Positives = 16/25 (64%)

Query: 139 LSGGQKVKASVVGYYDEYTDLAVLKI 163
LS GQ+V VV YDEY+ A L +
Sbjct: 50 LSVGQEVLVQVVDYDEYSQKASLSL 74

>ref|NP_721524.1| putative ABC transporter, phosphate-binding protein
[Streptococcus
mutans UA159]
Length = 287

Score = 26.6 bits (57), Expect = 1.4
Identities = 17/44 (38%), Positives = 21/44 (47%), Gaps = 1/44 (2%)

Query: 335 LPAASAGLKAGDVITKVGDTAVTSSTDLSALYSH-NINDTVKV 377
L A S + G IT VG TA+ + S + H NI TV V
Sbjct: 19 LAACSNWIDKGQSITSVGSTALQPLVEASSDEFGHANIGKTVNV 62

>ref|NP_722399.1| glucan-binding protein A, GbpA [Streptococcus mutans UA159]
Length = 565

Score = 26.2 bits (56), Expect = 1.8
Identities = 30/153 (19%), Positives = 54/153 (35%), Gaps = 12/153 (7%)

Query: 172 ATFADSSKLTIGEPAlAVGSPLGSQFANTATEGILSATSQRQVTLTQENGQTTNINAIQTD 231
AT +SS+ + E A S N + + S+ + + + G+ + A+
Sbjct: 55 ATVQESSEQPVTEAPAA-----DSSVENNSANAVKSSETAEAAEVSDGGRASQTEAVTNQ 109

ANNEX 5

Query: 232 AAINPGNSGGALINIEGQVIGITQSKITTEDGSTSVEGLGFAIPSNDDVNIINKLEADG 291
 + + G+ + + T+ A +ND + E DG
 Sbjct: 110 TNSEHHHPAEKATAVSGEAQSVQNAPSENAQQETAKTEPATAAENNDAAPTNSFFEKDG 169

Query: 292 K-----ISRPALGIRMVDLSQLSTN-DSSQLK 317
 K + A G + +D QL N D SQ+K
 Sbjct: 170 KWYYKKADGQLATGWQTIDGKQLYFNQDGSQVK 202

>ref|NP_721986.1| putative D-3-phosphoglycerate dehydrogenase [Streptococcus mutans

UA159]
 Length = 393

Score = 25.8 bits (55), Expect = 2.4
 Identities = 17/78 (21%), Positives = 32/78 (41%), Gaps = 3/78 (3%)

Query: 138 LLSGGQKVKASVVGYYDEYTDLAVLKISSEHVKDVATFADSSKLTIGEPAAVGSPLGSQF 197
 + + +++ +V+GYD Y + S HVK V D + I + PL +
 Sbjct: 151 IANDARRLGMMNVLGYPVSIETAWNISSHVKKRVNDLKD---IFENSDYITIHVPLNDET 207

Query: 198 ANTATEGILSATSRSQVTL 215
 NT + ++ T+
 Sbjct: 208 KNTFNADSFALMNKGTTI 225

>ref|NP_722066.1| putative 3-oxoacyl-(acyl-carrier-protein) synthase [Streptococcus

mutans UA159]
 Length = 410

Score = 25.8 bits (55), Expect = 2.4
 Identities = 27/136 (19%), Positives = 48/136 (35%), Gaps = 13/136 (9%)

Query: 136 DVLLSGGQKVKASVVGYYDEYTDLAVLKISSEHVKDVATF-ADSSKLTIGEPAAVGSPLG 194
 DV+L+GG + + +G + L L + + + F D + +GE A
 Sbjct: 184 DVILAGGSEASITKIGIGGFNALTALSTEDPARSAIPFDKDRNGFVMGEA----- 235

Query: 195 SQFANTATEGILSATSRSQVTLTQE-NGQTTNINAIQTDAAINPGNSGGALINIEGQVIGI 253
 A E + A R + E G +N +A G+ I + GI
 Sbjct: 236 ---AVLILESLEHAQKRGARILAEVVGYSNCDAYHMTTPTPDGSGAAKAIKLAINAEAGI 292

Query: 254 TQSKITTEDGSTSVE 269
 + ++ TS +
 Sbjct: 293 SPEEVNYVNAHGTSTQ 308

>ref|NP_722435.1| conserved hypothetical protein [Streptococcus mutans UA159]
 Length = 325

Score = 25.4 bits (54), Expect = 3.1
 Identities = 18/61 (29%), Positives = 27/61 (44%), Gaps = 12/61 (19%)

Query: 198 ANTATEG----ILSATSRSQVTLTQENGQTTNINAIQTDAAINPGNSGGALINIEGQVIGI 253
 A T+G L+AT + T+T G TT++ + G+ G I I GQ +

ANNEX 5

Sbjct: 258 ATNTDGESGTTLTATDKTYTTLAEGSTTSM-----LTVGSPSGVEITINGQKVDV 309

Query: 254 T 254

T

Sbjct: 310 T 310

>ref|NP_721103.1| phosphoenolpyruvate:sugar phosphotransferase system enzyme I,
PTS

system EI component [Streptococcus mutans UA159]
Length = 577

Score = 23.9 bits (50), Expect = 9.0
Identities = 19/104 (18%), Positives = 39/104 (37%), Gaps = 3/104 (2%)

Query: 210 SRQVTLTQENGQTTNINAIQTDAAINPGNSGGALINIEGQVIGITQSKITTEDGST-SV 268
+ +T +NG +N I INP A G+ +++ +D T +
Sbjct: 207 TNDITERVKNGDIVAVNGITGQVIINPTEDQIAEFKAAGETYAKQKAEWALLKDAETVTA 266

Query: 269 EGLGFAIPSNDDVNIINKLEADGKISRPAIGIRMVDLSQLSTND 312
+G F + +N + +E A+G+ + + + D
Sbjct: 267 DGKHFELAA--IGTPKDVGVNNGAEAVGLYRTEFLYMDSQD 308

>ref|NP_720786.1| hypothetical protein [Streptococcus mutans UA159]
Length = 411

Score = 23.9 bits (50), Expect = 9.0
Identities = 12/40 (30%), Positives = 19/40 (47%)

Query: 151 GYDEYTDLAVLKISSEHVKDVAFTADSSKLTIGEPPIAVG 190
GY +T + +S + K T AD LT+G+ + G
Sbjct: 301 GYAYFTSKDIKTVSEKSYKSDWTQADVDAITVGDSSSTGKG 340

Database: Completed Streptococcus mutans UA159
Posted date: Oct 1, 2003 10:43 PM
Number of letters in database: 579,702
Number of sequences in database: 1960

Lambda	K	H
0.308	0.128	0.338

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 35,974
Number of Sequences: 1960
Number of extensions: 1254

ANNEX 5

Number of successful extensions: 5
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 1
Number of HSP's that attempted gapping in prelim test: 5
Number of HSP's gapped (non-prelim): 1
length of query: 408
length of database: 577,947
effective HSP length: 81
effective length of query: 327
effective length of database: 419,835
effective search space: 137286045
effective search space used: 137286045
T: 11
A: 40
X1: 16 (7.1 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 42 (21.7 bits)
S2: 50 (23.9 bits)

ANNEX 6

BLASTP 2.2.6 [Apr-09-2003]

RID: 1065207742-9645-69613.BLASTQ3

Query=

(408 letters)

Database: Completed Streptococcus pneumoniae R6;

1,531,058 sequences; 495,743,110 total letters

Taxonomy reports

Sequences producing significant alignments:		Score (bits)	E Value
ref NP 359636.1	Serine protease [Streptococcus pneumoniae R6]	325	2e-90
ref NP 359374.1	Conserved hypothetical protein [Streptococ...	40	2e-04
ref NP 357681.1	Hypothetical protein [Streptococcus pneumo...	29	0.22
ref NP 357856.1	Alcohol dehydrogenase, propanol-preferring...	28	0.48
ref NP 357669.1	Conserved hypothetical protein [Streptococ...	27	1.4
ref NP 358044.1	EcoA type I restriction-modification enzym...	25	3.1
ref NP 359110.1	Penicillin-binding protein 2B [Streptococc...	25	5.3
ref NP 358390.1	6-phosphofructokinase I [Streptococcus pne...	24	6.9
ref NP 359031.1	Isochorismatase [Streptococcus pneumoniae R6]	24	6.9
ref NP 359032.1	Transcriptional pleiotropic repressor [Str...	24	9.0

Alignments

>ref NP 359636.1 Serine protease [Streptococcus pneumoniae R6]
Length = 397

Score = 325 bits (832), Expect = 2e-90
Identities = 167/284 (58%), Positives = 212/284 (74%), Gaps = 3/284 (1%)

Query: 107 EGSQVIYKKSGGDAYVVTNYHVIAGNSSLDVLLSGGQKVKASVVGDEYTDLAIVLKISSE 166
EGSQVIYKK+ +AY+VTN+HVI G S +D+ LS G KV +VG D ++D+AV+KISSE
Sbjct: 106 EGSQVIYKKNDKEAYIVTNNHVINGASKVDIRLSGDTKVPGEIVGADTFSDIAVVKISSE 165

ANNEX 6

Query: 167 HVKDVATFADSSKLTIGEPAlAVGSPGSGFANTATEGILSATSRQVTLTQENGQTTNIN 226
V VA F DSSKLT+GE AIA+GSPLGS++ANT T+GI+S+ +R V+L E+GQ +
Sbjct: 166 KVTTVAEFGDSSKLTVGETAIAIGSPGSEYANTVTQGIVSSLNRNVSLKSEdGQAISTK 225

Query: 227 AIQTDAAINPGNSGGALINIEGQVLGITQSKITTTEDGSTSVEGLGFAIPSNdVVNIINK 286
AIQTD AINPGNSGG LNI+GOVIGIT SKI T +G TSVEGLGFAIP+ND +NII +
Sbjct: 226 AIQTDTAINPGNSGGPLNIQGOVIGITSSKIAT--NGGTSVEGLGFAIPANDAINIEQ 283

Query: 287 LEADGKISRPALGIRMVDLSQLSTNDSSQLKLPXXXXXXXXXXXXXXXXLPAASAGLKAGD 346
LE +GK++RPALGI+MV+LS +ST+D +L +P +P A+ L+ D
Sbjct: 284 LEKNGKVTRPALGIQMVNLSNVSTSDIRRLNIPSNVTSGVIVRSVQSNMP-ANGHLEKYD 342

Query: 347 VITKVGDTAVTSSTDLSALYSHNINDTVKVTTYRDGKSNTADV 390
VITKV D + STDLSALY+H+I DT+K+TYR+GK T +
Sbjct: 343 VITKVDDKEIASSTDLSALYNHSIGDTIKITYRNGKEETTSI 386

>ref|NP_359374.1| Conserved hypothetical protein [Streptococcus pneumoniae R6]
Length = 345

Score = 39.7 bits (91), Expect = 2e-04
Identities = 19/48 (39%), Positives = 27/48 (56%)

Query: 342 LKAGDVITKVGDTAVTSSTDLSALYSHNINDTVKVTTYRDGKSNTAD 389
L D +T V D SS DL + S + D+VKVTY DG++ +A+
Sbjct: 146 LNISDVTAVNDQTFDSSKDLIDYVSSQKLGDSVKVTYEEDGQTKSAE 193

>ref|NP_357681.1| Hypothetical protein [Streptococcus pneumoniae R6]
Length = 320

Score = 29.3 bits (64), Expect = 0.22
Identities = 21/72 (29%), Positives = 33/72 (45%), Gaps = 5/72 (6%)

Query: 189 VGSPLGSQFANTATEGILSATSRQVTLTQENGQTTNINAIQTDAAINPGNSGGALINIEG 248
+ S S+F T + + ++ GQTT INA +A + N+ ++ IEG
Sbjct: 142 IASSYSSRFEEVILRLPKGRTLKGINISANRGQTTIINASLENATL---NTNSYILRIEG 198

Query: 249 QVIGITQSKITT 260
I SK+TT
Sbjct: 199 S--RIKNSKLTT 208

>ref|NP_357856.1| Alcohol dehydrogenase, propanol-preferring. [Streptococcus pneumoniae R6]
Length = 339

Score = 28.1 bits (61), Expect = 0.48
Identities = 18/73 (24%), Positives = 40/73 (54%), Gaps = 4/73 (5%)

Query: 109 SGVIYKSGGDAY--VVTNYHVIAGNSSLDVLLSGGQKVKASVVGDEYTDLAVLKISSE 166
+G+I +K+ G A+ VVT +A N ++D + +GG+ V + E +L+++K +
Sbjct: 221 AGLIKEKTdGGAHSAVVTAVSKVAFNQAVDSIRAGGRVVAVGLP--SEMMEISIVKTVLD 278

Query: 167 HVKDVATFADSSK 179

ANNEX 6

++ + + + K
Sbjct: 279 GIQVIGSLVGTRK 291

>ref|NP_357669.1| Conserved hypothetical protein [Streptococcus pneumoniae R6]
Length = 1161

Score = 26.6 bits (57), Expect = 1.4
Identities = 11/25 (44%), Positives = 16/25 (64%)

Query: 335 LPAASAGLKAGDVITKVGDTAVTSS 359
LP ++G K GD+ K GDT +T +
Sbjct: 53 LPEETSGTKEGDLSEKPGD TVLTQA 77

>ref|NP_358044.1| EcoA type I restriction-modification enzyme R subunit
[Streptococcus pneumoniae R6]
Length = 777

Score = 25.4 bits (54), Expect = 3.1
Identities = 18/66 (27%), Positives = 30/66 (45%), Gaps = 1/66 (1%)

Query: 119 DAYVVTNYHVIAGNSSLDVLLSGGQKVKASVVG YDEYTDLAVLKISSEHV KDVATFADSS 178
+ Y+VT+ V NS++ VL G+ + S+ Y L ++ + V AD
Sbjct: 588 EKYIVTDKQVTILNSTVQVLDENGKLITESLTDYTRKNILGSYATLNDFI-TVWHTADKK 646

Query: 179 KLTIGE 184
KL + E
Sbjct: 647 KLILDE 652

>ref|NP_359110.1| Penicillin-binding protein 2B [Streptococcus pneumoniae R6]
Length = 685

Score = 24.6 bits (52), Expect = 5.3
Identities = 14/47 (29%), Positives = 19/47 (40%)

Query: 190 GSPLGSQFANTATEGILSATS RQVTLTQENGQTTNINAIQTDAAINP 236
G G F+N A I T + + Q TN NA+ + NP
Sbjct: 602 GLTTGRAFSNGALVSISGKTGTAE SYVADGQQTNTNAVAYAPSDNP 648

>ref|NP_358390.1| 6-phosphofructokinase I [Streptococcus pneumoniae R6]
Length = 335

Score = 24.3 bits (51), Expect = 6.9
Identities = 14/49 (28%), Positives = 24/49 (48%)

Query: 246 IEGQVIGITQSKITTEDGSTSVEGLGFAIPSN DVVNIINKLEADGKIS 294
I G +GI K+ T+ EG F++ + + N EAD ++S
Sbjct: 280 IGGVAVGIRNEKMVENPILGTAE EGALFSLTAEGKIVVNNPHEADIELS 328

ANNEX 6

>ref|NP_359031.1| Isochorismatase [Streptococcus pneumoniae R6]
Length = 191

Score = 24.3 bits (51), Expect = 6.9
Identities = 13/31 (41%), Positives = 18/31 (58%), Gaps = 2/31 (6%)

Query: 163 ISSEHVKDVAATFADSSKLTIGEPAAVGSPL 193
IS ++ +D ADS KLT G PA A+ +
Sbjct: 6 ISIDYTEDFV--ADSGKLTAGAPAQAISDAI 34

>ref|NP_359032.1| Transcriptional pleiotropic repressor [Streptococcus pneumoniae R6]
Length = 262

Score = 23.9 bits (50), Expect = 9.0
Identities = 24/105 (22%), Positives = 40/105 (38%), Gaps = 22/105 (20%)

Query: 213 VTLTQENGQTTNINAIQTDAAINPGNSGGALINIEGQVIGITQSKITTTEDEGSTSVEGLG 272
VT+ + + A+ GN G ++ IGIT+S I
Sbjct: 176 VTMAVNTLSYSELRAVSAILGELNGNEGQLTASVIADRIGITRSVI----- 221

Query: 273 FAIPSNDDVNNIINKLEADGKISRPAIGIRMVDLSQLSTNDSSQLK 317
VN + KLE+ G I +LG++ L L ++ ++K
Sbjct: 222 -----VNALRKLESAGIIESRSLGMKGTYLKVLIIDIFEEVK 258

Database: Completed Streptococcus pneumoniae R6
Posted date: Oct 1, 2003 10:43 PM
Number of letters in database: 589,192
Number of sequences in database: 2043

Lambda	K	H
0.308	0.128	0.338

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 33,145
Number of Sequences: 2043
Number of extensions: 1151
Number of successful extensions: 4
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 1
Number of HSP's that attempted gapping in prelim test: 4
Number of HSP's gapped (non-prelim): 1
length of query: 408
length of database: 588,593

ANNEX 6

effective HSP length: 81
effective length of query: 327
effective length of database: 423,515
effective search space: 138489405
effective search space used: 138489405
T: 11
A: 40
X1: 16 (7.1 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 42 (21.7 bits)
S2: 50 (23.9 bits)

ANNEX 7

BLASTP 2.2.6 [Apr-09-2003]

RID: 1065207829-10461-370696.BLASTQ3

Query=

(408 letters)

Database: Completed Streptococcus pyogenes SSI-1;

1,531,058 sequences; 495,743,110 total letters

Taxonomy reports

Sequences producing significant alignments:			Score (bits)	E Value
ref NP_803122.1	putative serine protease [Streptococcus py...	311	2e-86	
ref NP_801300.1	putative alcohol dehydrogenase I [Streptoc...	32	0.030	
ref NP_802185.1	putative phage-related tail protein [Strep...	31	0.067	
ref NP_802392.1	putative tail protein, phage associated [S...	29	0.20	
ref NP_801584.1	putative transcriptional pleiotropic repre...	29	0.26	
ref NP_803013.1	putative transcriptional regulator [Strept...	25	2.8	
ref NP_802639.1	conserved hypothetical protein [Streptococ...	25	4.8	
ref NP_801305.1	50S ribosomal protein L4 [Streptococcus py...	25	4.8	

Alignments

>ref|NP_803122.1| putative serine protease [Streptococcus pyogenes SSI-1]
Length = 407

Score = 311 bits (797), Expect = 2e-86
Identities = 163/288 (56%), Positives = 207/288 (71%), Gaps = 5/288 (1%)

Query: 107 EGSQVIYKKSGGDAYVVTNYHVIAGNSSLDVLLSGGQKVKASVVGYYDEYTDLAIVLKISSE 166
EGSGVIY+K G AYVVTN-HVI G +++L++ G KV +VG D Y+DLAV+KISS+
Sbjct: 108 EGSQVIYRKDGNsAYVVTNNHVIDGAKRIEILMADGSKVVGELVGADTYSDLAIVKISSD 167

Query: 167 HVKDVATFADSSKLTIGEPAlAVGSPLGSQFANTATEGILSATSrqVTLTQENGQTnIN 226
+K VA FADS+KL +GE AIA+GSPLG+Q+AN+ T+GI+S+ SR VTL ENG+T + N

ANNEX 7

Sbjct: 168 KIKTVAEFADSTKLNVEVAIAIGSPLGTQYANSVTQGIVSSLSRTVTTLKNENGETVSTN 227

Query: 227 AIQTDAAINPGNSGGALINIEGQVIGITQSKITTEDGST----SVEGLGFAIPSNVNVN 282
 AIQTDAAINPGNSGGALINIEGQVIGI SKI++T GS +VEG+GFAIPS DV+

Sbjct: 228 AIQTDAAINPGNSGGPLINIEGQVIGINSSKISSTPTGSNGNSGAVEGIGFAIPSTDVIK 287

Query: 283 IINKLEADGKISRPALGIRMVDLSQLSTNDSSQLKLPXXXXXXXXXXXXXXXXLPAASAGL 342
 II +LE +G++ RPALGI MV+L+ LSTN SQ+ +P +P AS L

Sbjct: 288 IIKQLETNGEVIRPALGISMVNLNDLSTNALSQINIPSTVTGGIVVAEVKEGMP-ASGKL 346

Query: 343 KAGDVITKVGDTAVTSSTDLSALYSHNINDTVKVTYYRDGKSNTADV 390
 DVIT++ V S +DLQS+LY H+INDT+KVT+YR AD+

Sbjct: 347 AQYDVITEIDGKTVNSISDLQSSLYGHDINDTIKVTFYRGTTKKKADI 394

>ref|NP_801300.1| putative alcohol dehydrogenase I [Streptococcus pyogenes SSI-1]

Length = 282

Score = 32.0 bits (71), Expect = 0.030
 Identities = 21/71 (29%), Positives = 37/71 (52%), Gaps = 3/71 (4%)

Query: 110 GVIYKSGG-DAYVVVINYHVIAGNSSLDVLLSGGQKVKASVVGYYDEYTDLAVLKISSEHV 168
 G I +K+GG VVT +A N ++D + +GG V + EY +L+++K + +

Sbjct: 166 GYIQEKTGGAHVVTAVSKVAFNQIDSVRAGGTVVAVGLP--SEYMELSIVKTVLDGI 223

Query: 169 KDVATFADSSK 179
 K V + + K

Sbjct: 224 KVGSLVGTRK 234

>ref|NP_802185.1| putative phage-related tail protein [Streptococcus pyogenes SSI-1]

Length = 1307

Score = 30.8 bits (68), Expect = 0.067
 Identities = 48/213 (22%), Positives = 86/213 (40%), Gaps = 30/213 (14%)

Query: 153 DEYTDLAVLKISSEHV KDVATFADSSKLTIGEPAAVGSPLGSQFANTATEGILSATS RQ 212
 DE ++ K+S + ++ +A +S + I A A G T ILS +

Sbjct: 192 DETATVSYAKLS-QGIRQMAKELPASAVEIAHVAEAAGQ-----LGVKTDILSFSRTM 244

Query: 213 VTLTQENGQTTNINAIQTDAAINPGNSGGALINIEGQVIGITQSKITTEDGSTSVEGLG 272
 + L G++TN++A + +I + NI G + S+ + ++ G

Sbjct: 245 IDL----GESTNLSAEAAATSI-----AKIANITG----LASSEYSRFGSAVVAL-GNN 289

Query: 273 FAIPSNVNVNIIINKLEADGKISRPALGIRMVDLSQLSTNDSSQLKLPXXXXXXXXXXXXX 332
 FA D+V + N++ A GK++ G+ ++ L+T SS + +

Sbjct: 290 FATTEKDIVAMTNRIAASGKLA---GLTNQEMLALATAMSS-VGIEABAGGTAMTQSLS 344

Query: 333 XXLPAASAGLKAGDVITKVGDTAVTSSTDLSA 365
 A ++G GD + K A SS D A

Sbjct: 345 AIERAVASG---GDNLNKAQIANMSSADFARA 374

ANNEX 7

>ref|NP_802392.1| putative tail protein, phage associated [Streptococcus pyogenes

SSI-1]
Length = 1372

Score = 29.3 bits (64), Expect = 0.20
Identities = 34/146 (23%), Positives = 57/146 (39%), Gaps = 19/146 (13%)

Query: 220 GQTTNINAIQTDAAINPGNSGGALINIEGQVIGITQSKITTEDGSTSVEGLGFAIPSND 279
GQ+TN++A + ++I + NI G SK + S G F+ D
Sbjct: 254 GQSTNLSAEEAASSI-----AKIANITGLT-----SKEYSRFGSSVVALGNNFSTTERD 302

Query: 280 VVNIINKLEADGKISRPAIGRMVDLSQLSTNDSSQLKLPXXXXXXXXXXXXXXXXLPAAS 339
V+ + N++ A GK++ G+ ++ L+T SS +
Sbjct: 303 VIAMTNRIAASGKLA----GLTNQEMLALATAMSS----VGIEAEAGGTAMTQTLSAIET 354

Query: 340 AGLKAGDVITKVGDTAVTSSTDLQSA 365
A + G+ +TK A SS D A
Sbjct: 355 AVINGGEDLTAKFAQIANMSSKDFAKA 380

>ref|NP_801584.1| putative transcriptional pleiotropic repressor [Streptococcus pyogenes SSI-1]
Length = 260

Score = 28.9 bits (63), Expect = 0.26
Identities = 34/128 (26%), Positives = 52/128 (40%), Gaps = 26/128 (20%)

Query: 193 LGSQFANTATEGILSATSRQVTLTQENGQTTNINAIQTDAAIN--PGNSGGALINIEGQ 249
+G Q N TE L T R+ T T + + ++ AAI GN G ++
Sbjct: 154 VGIQLNLQQTEN-LEDTIRKQTAVNMAINTLSYSEMKAVAAILGELDGNRGLTASVIAD 212

Query: 250 VIGITQSKITTEDGSTSVEGLGFAIPSNDVVNIINKLEADGKISRPAIGRMVDLSQLS 309
IGIT+S I VN + KLE+ G I +LG++ L ++
Sbjct: 213 RIGITRSVI-----VNALRKLESAGIIESRSLGMKGYLKVIN 250

Query: 310 TNDSSQLK 317
++LK
Sbjct: 251 EGIFAKLK 258

>ref|NP_803013.1| putative transcriptional regulator [Streptococcus pyogenes SSI-1]
Length = 326

Score = 25.4 bits (54), Expect = 2.8
Identities = 21/79 (26%), Positives = 36/79 (45%), Gaps = 7/79 (8%)

Query: 112 IYKKSGGDAYVVVTNYHVIAGNSSLDVLLSGGQK-VKASVVGYDEYTDLAVLKISSEHVKD 170
IY +GG +++ YHV L + G + A V+ D++ +L+ S++ D
Sbjct: 138 IYPLAGGPHSHINAKYHVNTLVYRLARIFHGNSAFMNAMVIQEDKHLAKGILQ--SKYFND 195

Query: 171 VATFADSSKLT-----GEP 185
+ T D L + GEP
Sbjct: 196 ILTSWDQLDLALVGIGGEP 214

ANNEX 7

>ref|NP_802639.1| conserved hypothetical protein [Streptococcus pyogenes SSI-1]
Length = 574

Score = 24.6 bits (52), Expect = 4.8
Identities = 10/32 (31%), Positives = 20/32 (62%)

Query: 345 GDVITKVGDTAVTSSTDLSALYSHNINDTVK 376
G +I K D+ +TS + + AL++ +ND ++
Sbjct: 23 GVIIRKRNDSLITSLEERKQALFALPVNDEIE 54

>ref|NP_801305.1| 50S ribosomal protein L4 [Streptococcus pyogenes SSI-1]
Length = 207

Score = 24.6 bits (52), Expect = 4.8
Identities = 12/33 (36%), Positives = 18/33 (54%), Gaps = 1/33 (3%)

Query: 262 EDGSTSVEGLGFAIPSN-DVVNIINKLEADGKI 293
ED +VEGL FA P + +++ L D K+
Sbjct: 120 EDKFVAVEGLSFAAPKTAFAKVLALSIDTKV 152

Database: Completed Streptococcus pyogenes SSI-1
Posted date: Oct 1, 2003 10:43 PM
Number of letters in database: 534,258
Number of sequences in database: 1861

Lambda	K	H
0.308	0.128	0.338

Gapped		
Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 32,970
Number of Sequences: 1861
Number of extensions: 1177
Number of successful extensions: 3
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 1
Number of HSP's that attempted gapping in prelim test: 3
Number of HSP's gapped (non-prelim): 1
length of query: 408
length of database: 532,687
effective HSP length: 80
effective length of query: 328
effective length of database: 384,447
effective search space: 126098616
effective search space used: 126098616

ANNEX 7

T: 11
A: 40
X1: 16 (7.1 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 42 (21.7 bits)
S2: 50 (23.9 bits)

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htrA bacteria

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Site-directed mutagenesis of the **HtrA** (DegP) serine protease, ...
... An identical effect was observed when His105 was mutated. The mutated **HtrA**

were unable to suppress thermosensitivity of the **htrA bacteria**. ...[www.ncbi.nlm.nih.gov/entrez/query.fcgi?](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=PubMed&list_uids=96001242&dopt=Abstract)[cmd=Retrieve&db=PubMed&list_uids=96001242&dopt=Abstract](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=PubMed&list_uids=96001242&dopt=Abstract) - Similar pages

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